

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 18, 2004, 17:11:45 ; Search time 147.679 Seconds  
(without alignments)

3569.936 Million cell updates/sec

Title: US-09-373-658C-2

Perfect score: 5189  
Sequence: 1 MGNARAPGSRSGFVPTLL.....CDPLKKPKHFIDCTMAECS 950

Scoring table:

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Zgapop 6.0, Zgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/prodata/2/ina/PTCUS\_COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5189	100.0	4576	4	US-09-130-491-1
2	5176	99.7	4858	4	US-09-392-184-1
3	5174	99.7	3889	4	US-09-568-559-1
4	4287	82.6	3706	4	US-09-484-970B-58
5	3947	76.1	2184	4	US-09-445-023A-2
6	3677	70.9	2184	4	US-09-445-023A-13
7	2284.5	44.0	3638	4	US-09-369-364A-8
8	2176.5	41.9	3126	4	US-09-392-184-7
9	2168	41.8	4192	4	US-09-122-126B-1
10	2168	41.8	4192	4	US-09-634-286A-1
11	1931	37.2	3250	4	US-09-122-126B-14
12	1931	37.2	3250	4	US-09-634-286A-14

13	1918	37.0	3002	4	US-09-369-364A-1	Sequence 1, Appl
14	1756.5	33.9	5804	4	US-09-369-364A-12	Sequence 12, Appl
15	1611	31.0	2625	4	US-09-369-364A-14	Sequence 14, Appl
16	1405.5	27.1	2114	4	US-09-130-491-7	Sequence 7, Appl
17	1320.5	25.4	5357	4	US-09-392-184-5	Sequence 5, Appl
18	1296.5	25.0	3675	4	US-09-930-872-3	Sequence 3, Appl
19	1296.5	25.0	4042	4	US-09-930-872-5	Sequence 5, Appl
20	1213.5	23.4	2727	4	US-09-963-791-1	Sequence 1, Appl
21	1210.5	23.3	3218	4	US-09-369-364A-6	Sequence 6, Appl
22	1198	23.1	3885	4	US-09-369-364A-16	Sequence 16, Appl
23	1152.5	22.2	2274	4	US-09-963-791-23	Sequence 23, Appl
24	1134	21.9	6592	4	US-09-491-522-1	Sequence 1, Appl
25	1118	21.5	4580	4	US-09-491-522-8	Sequence 8, Appl
26	1065.5	20.5	3160	4	US-09-963-791-25	Sequence 25, Appl
27	1041.5	20.1	1520	4	US-09-369-364A-3	Sequence 3, Appl
28	1037.5	20.0	2848	4	US-09-369-364A-4	Sequence 4, Appl
29	966.5	18.6	2450	4	US-09-491-522-2	Sequence 2, Appl
30	965.5	18.6	2450	4	US-09-491-522-9	Sequence 9, Appl
31	780	15.0	1770	4	US-09-963-791-11	Sequence 11, Appl
32	719	13.9	1317	4	US-09-963-791-21	Sequence 21, Appl
33	716.5	13.8	739	4	US-09-369-364A-10	Sequence 10, Appl
34	641	12.4	1810	4	US-09-833-381-1056	Sequence 1056, Ap
35	612.5	11.8	703	4	US-09-392-184-6	Sequence 6, Appl
36	601	11.6	5720	4	US-09-800-729-18	Sequence 18, Appl
37	592.5	11.4	1524	4	US-09-963-791-9	Sequence 9, Appl
38	574.5	11.1	1803	4	US-09-369-364A-20	Sequence 20, Appl
39	531.5	10.2	1071	4	US-09-963-791-19	Sequence 19, Appl
40	508	9.8	2023	4	US-09-491-522-6	Sequence 6, Appl
41	498	9.6	1407	4	US-09-963-791-5	Sequence 5, Appl
42	486	9.4	1476	4	US-09-930-872-1	Sequence 1, Appl
43	440	8.5	852	4	US-09-800-729-54	Sequence 54, Appl
44	438	8.4	3559	4	US-09-800-729-53	Sequence 53, Appl
45	437	8.4	954	4	US-09-963-791-15	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1

US-09-130-491-1  
; Sequence 1, Application US/09130491  
; Patent No. 6416974  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Goodearl, Andrew D.J.  
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
; FILE REFERENCE: 09404/041001  
; CURRENT APPLICATION NUMBER: US/09130491  
; CURRENT FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: US 60/058108  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: US 60/054,961  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4676  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (460)...(3360)  
US-09-130-491-1

#### Alignment Scores:

Pred. No.: 0  
Score: 5189.00  
Matches: 4676  
Conservative: 950  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

US-09-373-658C-2 (1-950) x US-09-130-491-1 (1-4676)

*no biotech data or for TANGO  
no bio tech data or for TANGO  
not correct invention, or for TANGO  
60/054, 966*

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
DB 511 ATGGGGAACGGGAGCGGCTCCGGGCTCTCGAGCGTTTGGGCCCTACCCACGCTGCTG 570  
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
DB 571 CTGCTCGCCGCGCGCTACTGCGCGTGTGCGAGCGACTCGGGCGCCCTCCGAGGAGAC 630  
QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrArgLeuArg 60  
DB 631 GAGGAGCTAGTGGTCCGAGCTGAGCGCGCCCGGACACGGGACCGCGCTCCGC 690  
QY 61 LeuHisAlaPheAspGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80  
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QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120  
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QY 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140  
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QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160  
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QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 180  
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QY 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280  
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QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
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QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
DB 1531 AGACAGGACTTGTGGGGTCCAGACATGTGATCTCTGGGATGGCTGATGTTGGAACT 1590  
QY 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380

DB 1591 GTGTGTGATCCGAGCAGAGCTGCTCGTCTATACAGATGATGTTTCAAGAGCTGCCTTC 1650  
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QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
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QY 421 AspHisSerGlnProTyrProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
DB 1771 GACCACAGCAGCCTTGGTCTCTCTGAGTGCCTACATGATTACATCATTTCTCGATAAT 1830  
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QY 621 GlySerGlyProAlaValGluTyrIleProLysTyrAlaGlyValSerProLysAspArg 640  
DB 2371 GGGAGTGGGCTGGGTGGATGGATTCCTCAAGTACGCTGCGCTCTCCACAAAGGACAGG 2430  
QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyThrPhePheValLeuGlnProLysVal 660  
DB 2431 TGCAAGCTCATCTGCCAAGCAAGGCATTTGGCTACTTCTTCGTTTTTGCAGCCCAAGGTT 2490  
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QY 681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700  
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DB 2611 GGGGGAATGATCTACTTGTAAATAAATATCAGGATCAGTACTACTAGTCGAAACCTGGA 2670  
QY 721 TyrHisAspIleIleThrIleProThrGlyValaThrAsnIleGluValLysGlnArgAsn 740

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Db      2731  CAGAGGGGATCCAGGAACAATGGCAGCTTCTTGCCATCAAGCTCTGATGACATAT 2790
QY      761  IleLeuAsnGlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrIysGlyVal 780
Db      2791  ATTCTTAATGGTGACTACATCTTGTCCACCTTAGACGACAGACATATGTACAAAGGTGT 2850
QY      781  ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProIleu 800
Db      2851  GTCCTTGAGGTACAGCGCTCTCTCGCGCATTTGGAAGAATTCGCAGCTTTTAGCCCTCTC 2910
QY      801  LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProIysIleIys 820
Db      2911  AAGAAGCCCTTCACCATCCAGGCTCTTACTGTGGGCAATGCTCTCGACCTAAATTA 2970
QY      821  TyrThrTyrPheValIysIysIysGluSerPheAsnAlaIleProThrPheSerAla 840
Db      2971  TACACCTACTTCTGTAAGAAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 3030
QY      841  TrpValIleGluGluTrpGlyGluCysSerIysSerCysGluLeuGlyTrpGlnArg 860
Db      3031  TGGGTCATTGAAGAGTGGGGCGAATGTTCTAAGTCTATGTAATTGGTTGGCAGAGA 3090
QY      861  LeuValGluCysArgAspIleAsnGlnPheAlaSerGluCysAlaIysGluValIys 880
Db      3091  CTGGTAGAATGCGAGACATTAATGAGACAGCCCTGCTTCGAGTGTGCAAAAGGAAG 3150
QY      881  ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db      3151  CCAGCGACGACAGACCTTGTGCAGACCATCCCTGCCCCAGTGCAGTGGGGAGTGG 3210
QY      901  SerSerCysSerLysThrCysGlyLysGlyTyrIysLysArgSerLeuLysCysLeuSer 920
Db      3211  TCATCATGTTCTTAGACCTGTGGGAAGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCC 3270
QY      921  HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysIysProIysHisPhe 940
Db      3271  CATGATGAGGGGGTGTATCTCATGAGAGCTGTGTATCTTTAAAGAAACCTTAAACATTT 3330
QY      941  IleAspPheCysThrMetAlaGluCysSer 950
Db      3331  ATAGACTTTTGCACATGGCAGAAATGCAGT 3360

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## RESULT 2

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US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(4858)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A,T,C or G
US-09-392-184-1

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## Alignment Scores:

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Pred. No.: 0          Length: 4858
Score: 5176.00        Matches: 950
Percent Similarity: 99.89%      Conservative: 0
Best Local Similarity: 99.89%    Mismatches: 0
Query Match: 99.75%             Indels: 1
DB: 4                          Gaps: 0

US-09-373-658C-2 (1-950) x US-09-392-184-1 (1-4858)

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QY      21  LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerSerGluGluAsp 40
Db      565  CTGCTCGCGCGCGCTACTGCGCTGTGCGACGCACTCGGGGCGCCCTCCGAGAGGAGAC 624
QY      41  GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrArgIleuArg 60
Db      625  GAGGAGCTAGTGGTGGCGGAGCTGGAGCGCCCGCGGACACCGGACACCGCTCCGCG 684
QY      61  LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
Db      685  CTGCACGCTTTGACGACGCTGATCTGAGGTGGCGCCCGCAGCAGAGCTTTTGGCG 744
QY      81  ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db      745  CCGGCTTCACTCCAGAACTGGGGCGCAATCCGGGTCCGAGACCGCGCTTCCGGAA 804
QY      101  ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db      805  ACCGCTTGGCGCACTGCTTCTACTCGGCACTCCGATGATGCGCATCCAGCTCGCTGCC 864
QY      121  AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db      865  GCGCTCAGCTCTCGAGGGCGTCCGGCGGCGCTTCTACCTGCTGGGGAGGCGTATTTC 924
QY      141  IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysPro 160
Db      925  ATCCAGCGCTGCCCGCGCGCAGCGCGCTCCGCCACCGCGCCCGCGGGGAGAAAGCCG 984
QY      161  ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
Db      985  CCGGCACTACAGTTCCACCTCTCGGGCGGATCGGCGAGGCGAGCTAGGGCGGACG 1044
QY      181  CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db      1045  TGGGGGCTCGTGGACGACGAGCCCGCGCCGACTGGGAAAGCGGAGACCGAAGACGAGAC 1104
QY      201  GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db      1105  GAAGGACTGAGGGCGGAGGAGGCGCTCAGTGTGCGCGAGGAGCCCGGCACTGCCAA 1164
QY      221  GlyValGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
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QY      241  ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db      1225  CGCTATGTGGAAACCACTGCTTGTGGCAGACCACTGCGATGGCAGATTCCACGGCAGTGT 1284
QY      261  LeuLysHisTyrIleuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrIysHisProse 280
Db      1285  CTAAGCATTACCTTCTCAACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCAG 1344
QY      280  rIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnIly 300
Db      1345  CATTCGTAAATTCAGTTAGCTGTGGTGGTGAAGATCTTGGTTCATCCACCATGAACAGAA 1404
QY      300  sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnIly 320
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QY 340 rArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyTh 360  
DB 1525 CAGACAGGACTTGTGTGGTCCAGACATGTGATCTCTTGGATGGCTGTGTGGAC 1584  
QY 360 rValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPh 380  
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QY 380 eThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaAlaGlnCys 400  
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DB 1765 GACACACAGCCAGCCTTGTCTCTCTGCAAGTCCAGATGATGGGTCAATGCTTTCCAACT 1824  
QY 440 nGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLe 460  
DB 1825 TGGTCATGGGAATGTTTATGGCAAGCCTCAGATCCATACAGCTCCAGGCGATCT 1884  
QY 460 uProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerIly 480  
DB 1885 CCTTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1944  
QY 480 shiCysProAspAlaAlaserThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
DB 1945 ACACCTGCCCTGATGAGCCAGCAGACATGATGATGATGATGATGATGATGATGATGAT 2004  
QY 500 yValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520  
DB 2005 GGT 2064  
QY 520 yLysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPr 540  
DB 2065 GAAATGT 2124  
QY 540 oPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
DB 2125 TTTTCATGGAACTGGGGAATGTGGGGCTTGGGGACACTGTTCCAGAACGTGGGTGG 2184  
QY 560 yGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTy 580  
DB 2185 AGGAGTCAGTACAGATGAGGAAATGCAACCCAGTCCCAAGAAATGGAGGAAATG 2244  
QY 580 rCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAs 600  
DB 2245 CTGTGAAGGCAACAGGTGCGCTACAGATCTGTAACTTCCAGGACTGTCCAGACATAA 2304  
QY 600 nGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPh 620  
DB 2305 TGGAAACACCTTATAGAGGAAACATGTGAAGCAACACCAAGCAATTTTCAAAAGCTTCT 2364  
QY 620 eGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspAr 640  
DB 2365 TGGAGTGGGCTGCGGTGGAAATGATTTCCCAAGTACGTGGCTCTCCACCAAGAGCAG 2424  
QY 640 qCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVa 660  
DB 2425 GTGCAAGCTCATCTGCCAAGCAAGGCAATGGGTACTTCTTCTTGTGAGCCCAAGGT 2484  
QY 660 lValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVa 680  
DB 2485 TGTAGATGGTACTCATGTAGTACCCAGATTCACCTCTGTCTGTGTGAGGACAGTGTGT 2544  
QY 680 lLysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCy 700

DB 2545 AAAAGCTGGTGTGTGATCGCATAGACTCCAAAAGAAAGTTTGATAAATGTGTGTGTG 2604  
QY 700 sGlyGlyAsnGlySerThrCysLysLysLysLysLysLysLysLysLysLysLysLys 720  
DB 2605 CGGGGAAATGGATCTACTTGTAAAAAATATCAGGATCAGTTCTAGTGTGAAAAACCTGG 2664  
QY 720 yfHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAs 740  
DB 2665 ATATCATGATATCATCAATTCACATTCGAACTGGAGCCACCAACATCGAAGTGAACGCGAA 2724  
QY 740 nGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaIleAspGlyThrTy 760  
DB 2725 CAGAGGGGATCCAGAGAAATGGAGCTTCTTGGCCATCAAGCTGTGTGATGGCACATA 2784  
QY 760 rIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVa 780  
DB 2785 TATCTTAAATGGTACTACACTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGT 2844  
QY 780 lValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLe 800  
DB 2845 TGTCTTAGGTACAGCGCTCTCTCGGGCAATGGAAAGAAATTCGACCTTTAGCCCTCT 2904  
QY 800 uLysGlyProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLy 820  
DB 2905 CAAGAGCCCTTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAATTA 2964  
QY 820 sTyrThrTyrPheValLysLysLysLysLysLysLysLysLysLysLysLysLys 840  
DB 2965 ATACACCTACTTCTGTAAAGAGAGAAAGAAATCTTTCAATGCTATCCCACTTTTCAGC 3024  
QY 840 aTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgAr 860  
DB 3025 ATGGGTCAATGAAGAGTGGGGCGAATGTTCTAAGTCAATGNAATGGTGGCAGAGAG 3084  
QY 860 gLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluVally 880  
DB 3085 ACTGGTGAATGCCAGACATTAATGACAGCCTGTCTCCAGTGTGCCAAGAAAGTGA 3144  
QY 880 sProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTr 900  
DB 3145 GCCAGCAGCACACAGACTTGTGCAGACCACTCCCTGCCCCAGTGGCGAGGTG 3204  
QY 900 pSerSerCysSerLysThrCysGlyLysGlyLysLysLysLysLysLysLysLysLys 920  
DB 3205 GTCATCATGTTCTAAGACCTGTGGAGGGTTTACAAAAAAGAAAGCTTGAAGTGTCTGTC 3264  
QY 920 xHisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPh 940  
DB 3265 CCATGATGGAGGGTGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAACATTT 3324  
QY 940 eIleAspPheCysThrMetAlaGluCysSer 950  
DB 3325 CATAGACTTTTGCACAAATGGCAGATGCACT 3355

## RESULT 3

US-09-568-559-1  
; Sequence 1, Application US/09568559  
; Patent No. 6649377  
; GENERAL INFORMATION:  
; APPLICANT: Klonowski, Paul  
; APPLICANT: Allard, John  
; APPLICANT: Heller, Renu  
; APPLICANT: van Wart, Harold  
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid  
; TITLE OF INVENTION: Compositions Encoding the Same  
; FILE REFERENCE: ROCH-002  
; CURRENT APPLICATION NUMBER: US/09/568,559  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: 60/133,343  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0



! SEQ ID NO 1  
! LENGTH: 3889  
! TYPE: DNA  
! ORGANISM: human  
US-09-568-559-1

## Alignment Scores:

Pred. No.: 0 Length: 3889  
Score: 5174.00 Matches: 948  
Percent Similarity: 99.79% Conservative: 0  
Best Local Similarity: 99.79% Mismatches: 2  
Query Match: 99.71% Indels: 0  
DB: 4 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-568-559-1 (1-3889)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
DB 59 ATGGGGAACCGGAGCGGGCTCCGGGCTCTCGAGCTTTGGGCGGTACCCACGCTGCTG 118  
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
DB 119 CTGCTCCGCGGGGCTACTGGCGGTCTCGAGCGCACTCGGGCGCCCTCCGAGGAGAC 178  
QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60  
DB 179 GAGGAGCTAGTGTGTCGGAGCTGGAGCGCGCCCGGGACACCGGACCGGCTCCGC 238  
QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerPheLeuAla 80  
DB 239 CTGACACGCTTTGACACGACGCTGATCTGGAGCTGCGGCGCGACAGCAGCTTTTGGCG 298  
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerGluThrProLeuProGlu 100  
DB 299 CCGGCTTCACGCTCCAGACGTTGGGCGCAATCCGGGTCGAGAGCGCGCTTCGGAA 358  
QY 101 ThrAspLeuAlaHisCysPheThrSerglyThrValAsnGlyAspProSerSerAlaAla 120  
DB 359 ACCGACCTGCGGCACTGCTTACTCTCGGCACTGATCGGATCCGATCCGCTGCGCTGCC 418  
QY 121 AlaLeuSerLeuGlyGluValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPhe 140  
DB 419 GCGCTCAGCTCTGCGAGGCGGTGCGGCGGCGCTTCTACCTGCTGGGGAGGCGTATTC 478  
QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160  
DB 479 ATCCAGCGCTGCCCGCGCCAGCGAGCGCTTCGCCACCGCGCCCGCGGAGAGCGG 538  
QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 180  
DB 539 CCGGACCACTACAGTTTCCACCTCTCGGCGGAAATCGGAGGCGGACGCTCGGCGGACG 598  
QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200  
DB 599 TCGGGGTCTGTGACGACGAGCGCCCGCGGCTCGGAAAGCGGAGCCGAGACGAGGAC 658  
QY 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220  
DB 659 GAAGGACTCAGGCGGAGGACGAAGGGGCTCAGTGTGTCGCGGACCGCCGACCTGCAA 718  
QY 221 GlyValGlnProThrGlyThrGlySerIleArgGlyLysArgPheValSerSerHis 240  
DB 719 GCGGTAGACAGCCCAAGAACTGGAAGCATAGAAAGAGCGATTGTGTCCAGTCAC 778  
QY 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260  
DB 779 CGCTATGTGGAACCATGCTTGTGGCAGACCATGTCGATGCGAGAAATTCACGCGCAGTGT 838  
QY 261 LeuLysHisThrLeuLeuThrPheSerValAlaAlaArgLeuTyrLysHisProSer 280  
DB 839 CTAAGACATTTACCTTCTCAGCTTGTTCGCTGGCAGCCGACGATTGTACAAACACCCGAC 898  
QY 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300

DB 899 ATTCGTAATTTCAGTTAGCCTGGTGGTGAAGATCTTGGTTCATCCACGATGACAGAAG 958  
QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320  
DB 959 GGGCCGGAAGTGACCTCCAAATGCTGCCCTCCTCTCTCGGAACCTTTTGCAACTCGGAGAAG 1018  
QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
DB 1019 CAGCACAAACCCAGTACCGGATGACGAGTGCAGAGCACTATGACACAGCAATCTCTTTCACC 1078  
QY 341 ArgGlnAspLeuGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
DB 1079 AGACAGACTTGTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAAT 1138  
QY 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaIlePhe 380  
DB 1139 GTGTGTGATCCGAGCAGAGAAGCTCTCCGTCATAGAGATGATGTTTACAAGCTGCTTC 1198  
QY 381 ThrThrAlaHisIleLeuLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400  
DB 1199 ACCACAGCCCATGAATAGGCCACGCTTTTAAATCATGATGCCATGATGATGATGATGATGAT 1258  
QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
DB 1259 GCCAGCTTTAATGGTGTGAACCCAGGATTCACCATGATGCGCTCAATGCTTTCACACTG 1318  
QY 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
DB 1319 GACCACAGCAGCCTTGGTCTCTCTTGCAGTGGCTACATGATATACATCATTTCTGGGTAAT 1378  
QY 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
DB 1379 GGTATGGGGAAGTTTGTATGGACAGCTCAGATCCCATACAGTCCGAGCGATCTC 1438  
QY 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
DB 1439 CCTGGCACCTCTGATCGATGCCAACCGGAGTGCAGTTTACATTTGGGAGGACTCCAA 1498  
QY 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
DB 1499 CACTGCCCCCTGATGACGCCAGCACATGTAGACCTTGTGTGTGTACCGGACCTCTGGTGG 1558  
QY 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520  
DB 1559 GTGCTGTGTGTCAACACCAACACATTCCTCCGTGGGCGATGGCACCACTGTGAGAGGG 1618  
QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
DB 1619 AAATGTGTATCAACGGCAAGTGTGTGAACCAAAACCCACAGAAAGCATTTTGTATACGCT 1678  
QY 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
DB 1679 TTTTCATGGAAGCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACGTGCGGTGGA 1738  
QY 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580  
DB 1739 GGAGTCCAGTACACCATGAGGGAATGTGAACCCAGTCCCAAGAAATGGAGAAAGTAC 1798  
QY 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
DB 1799 TGTGAAGGCAACAGAGTGCCTACAGATCTGTAACTTTGAGACTGTCCAGACAATAAT 1858  
QY 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
DB 1859 GGAAAAACCTTTAGAGAGGAACAAATGTGAAGCACACACGAGTTTCAAAGCTTCTCTT 1918  
QY 621 GlySerGlyProAlaValGlnTrpIleProLysTyrAlaGlyValSerProLysAspArg 640  
DB 1919 GGGAGTGGGCGCTCGCGTGAATGGATTCCCAAGTACGCTGGCGCTCCACCAAGGACAGG 1978  
QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660

Db 1979 TGAAGCTCATCTGCCAAGCCAAAGGCAATGGCTACTTCTCGTTTTCAGCCCCAAGGTT 2038  
QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680  
Db 2039 GTAGATGGTACTCCATAGCCAGATCCACCTCTGCTGTGTGCAAGGACAGTGTGTA 2098  
QY 681 LysAlaGlyCysAspArgIleLeuAspSerLysLysPheAspLysCysGlyValCys 700  
Db 2099 AAGCTGGTGTGTGATCGCATAGCACTCCAAAAGAGTGTGATAAATGTGGTGTTC 2158  
QY 701 GlyGlyAsnGlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGly 720  
Db 2159 GGGGGAATGGATCTACTGTGTAATAAATATATCAGATCAGTACTAGTGCAGAACTGGA 2218  
QY 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740  
Db 2219 TATCATGATATATCATCAAAATTCACCTGGAGCCCAACATCGAAGTGAAGACAGCGAAG 2278  
QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAspGlyThrTyr 760  
Db 2279 CAGAGGGATCCAGGACATAGGAGCTTCTTGCCATCAAGCTCTGATGGACATAT 2338  
QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyVal 780  
Db 2339 ATTCTTAATGGTGACTACACTTGTCCACCTTAGAGCAAGACATATATGACAAAGTGT 2398  
QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800  
Db 2399 GTCITGAGGTACAGCGCTCTCTGCGCATTTGGAAGATTCGAGCTTTAGCCCTCTC 2458  
QY 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820  
Db 2459 AAAGAGCCCTTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATA 2518  
QY 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840  
Db 2519 TACACCTACTCTGTAAGAGAGAGAGGAATCTTTCATGCTATCCCCACTTTTCAGCA 2578  
QY 841 TrpValIleGluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860  
Db 2579 TGGGTCAITGAAGAGTGGGGCAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAGA 2638  
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProLysArgGluCysAlaLysGluValLys 880  
Db 2639 CTGTAGATGTCGAGACATTAATGGACAGCTCTCTCCGAGTGTGCAAGAGAGTCAAG 2698  
QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900  
Db 2699 CCAGCCAGCACCAACCTTGTGCAAGACATCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2758  
QY 901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920  
Db 2759 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2818  
QY 921 HisAspGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940  
Db 2819 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTAAACATTT 2878  
QY 941 IleAspPheCysThrMetAlaGluCysSer 950  
Db 2879 ATAGACTTTTGACAAATGGCAGATGCACT 2908

## RESULT 4

US-09-484-970B-58  
; Sequence 58, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmuth, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B

; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 58  
; LENGTH: 3706  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 007074.1  
; NAME/KEY: unsure  
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681  
; OTHER INFORMATION: a, c, g, or other  
US-09-484-970B-58

## Alignment Scores:

Pred. No.: 0 Length: 3706  
Score: 4287.00 Matches: 777  
Percent Similarity: 99.87% Conservatives: 0  
Best Local Similarity: 99.87% Mismatches: 0  
Query Match: 82.62% Indels: 1  
DB: 4 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-484-970B-58 (1-3706)

QY 174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193  
Db 3 CAGGGCAGCTAGCGGCACGTGCGGGTCTGTGGACGACGAGCCCGCGGCTGGGAAA 62  
QY 194 AlaGluThrGluAspGluAspGluGlyThrGluGlyLysAspGluGlyProGlnTrpSer 213  
Db 63 GCGGAGACCGAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 122  
QY 214 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 233  
Db 123 CCAGGAGCCCGGCACTGCAAGGCGTAGGACAGCCCAAGGAACTGGAAGCATAGAAAG 182  
QY 234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253  
Db 183 AAGCGATTTGTGTCAGTCAACCGCTATGTGGAAACCATGCTTGTGGCAGACCACTGATG 242  
QY 254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 273  
Db 243 GCAGAAATTCACGCGCAGTGTCTAAAGCATTAACCTTCTCACGTTGTTTTCGGTGGCAGCC 302  
QY 274 ArgLeuTyrIleHisProSerIleArgAsnSerValSerLeuValValValLysIleLeu 293  
Db 303 AGATTGTACAAACACCCAGCATTCGTAATTCAGTTAGCTGTGTGTGTGTGAAGATCTTG 362  
QY 294 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 313  
Db 363 GTCATCCAGATGAACAGAGAGGCGCGGAAGTGACCTCCAAATGCTGCCCTCACTCTGCGG 422  
QY 314 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333  
Db 423 AACTTTTGCACTGGCAGAGAGCAGACAAACCCAGTGACCGGATGACAGAGCACTAT 482  
QY 334 AspThrAlaIleLeuPheThrArgGlnAspLeuLysGlySerGlnThrCysAspThrLeu 353  
Db 483 GACACAGCAATCTTTTTCACAGACAGAGACTTGTGTGGGTGCCAGACATGTGATACTCT 542  
QY 354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373  
Db 543 GGGATGGCTGATGTGTGAACCTGTGTGTATCCGAGCAGAAAGCTGCTCCCTCATAGAAGAT 602  
QY 374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393  
Db 603 GATGTTTACAGAGCTGCTTCCACAGCCCATGATTAATAGGCCACGCTGTTTAACATGCCA 662  
QY 394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413  
Db 663 CATGATGATGCAAGCAGTGTGCCAGCCTTAATGTGTGTGAACAGGATTTCCACATGATG 722

414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTyrProCysSerAlaTyrMet 433  
 723 GCCTCATGCTTCCAACTGGACACAGCCCTTGGTCTCTTGCAGTGCCTACATG 782  
 434 IleThrSerPheLeuAspGlnGlyHisGlyGluCysLeuMetAspGlnPro 453  
 783 ATTACATCATTTCTGGATATGCTGATGGGAATGTTGATGACCAAGCTCAGAATCC 842  
 454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 473  
 843 ATACAGCTCCAGGCGATCTCCCTGGACCTCTGATGATGCCAACCGGAGTGCAGTTT 902  
 474 ThrPheGlyCysAspSerLysHisCysProAspAlaAsnSerThrCysSerThrLeuTyr 493  
 903 ACATTTGGGAGGACTCCAAACACTGCCCGATGCAGCCAGCACATGTAGCCTTTGTG 962  
 494 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTyrAlaAsp 513  
 963 TGTACCGGACCTCTCTGGTGGGGTCTGGTGTGCAACCAACACTTCCCGTGGGGAT 1022  
 514 GlyThrSerCysGlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLysThrAsp 533  
 1023 GGCACCACTGTGGAGAGGGAATGTGTATCAACGGCAGTGTGTGAACAACCGAC 1082  
 534 ArgLysHisPheAspThrProPheHisGlySerTyrGlyMetTyrProTyrGlyAsp 553  
 1083 AGAAAGCATTTTCATCGCTTTTCATGGAAGCTGGGGAATGTGGGGCTTTGGGAGAC 1142  
 554 CysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 573  
 1143 TGTTCAGAAAGCTGCGTGGAGAGTCCAGTACAGATGAGGGATGTGCAACCACTG 1202  
 574 ProLysAsnGlyCysGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593  
 1203 CCAAGATATGAGGGAAGTACTGTGAAGGCACAAACGAGTGGCTTACAGATCTCTGAACCT 1262  
 594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHis 613  
 1263 GAGGACTGTCCAGACATATGAAACCTTTAGAGAGGAACAATGTGAAGCACACAC 1322  
 614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrPheProLysTyrAla 633  
 1323 GAGTTTCAAAAGCTTCTTTGGAGTGGGCTGGGTGGATGGATGCCCAAGTAGCT 1382  
 634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653  
 1383 GCGCTCTCAAAAGACAGGTGCAAGCTCATCTGCCAGCCAAAGGCTTGGCTACTTC 1442  
 654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673  
 1443 TTGCTTTTCAGCCCAAGTGTAGATGTGTACTCCATGTAGCCAGATCCACCTCTGTC 1502  
 674 CysValGlnGlyCysValLysAlaGlyCysAspArgIleAlaAspSerLysLys 693  
 1503 TGTGTCAAGGACAGTGTGTAAGCTGTTGTGATCGCATCATAGACTCCAAAAAGAG 1562  
 694 PheAspLysCysGlyValCysGlyValAsnGlySerThrCysLysLysIleSerGlySer 713  
 1563 TTGATATAATGTGGTGTTCGGGGGAATGATCTACTTTGTAATAAATAATACAGATCA 1622  
 714 ValThrSerAlaLysProGlyTyrHisAspIleThrIleProThrGlyValaThrAsn 733  
 1623 GTTACTAGTCAAAACCTGGATATCATGATATCATCAATTCCAATTCGAGCCACCAAC 1682  
 734 IleGluValLysGlnArgGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIle 753  
 1683 ATCGAAGTGAACAGCGGAACAGAGGGGATCCAGGAACAATGGGCAGCTTCTTGGCAT 1742  
 753 elysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGly 773  
 1743 CAAGCTCTGATGGACATATATCTTAATGTGACTACACTTGTCCACCTTAGACCA 1802  
 773 nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerAlaAlaLeuGluArg 793

1803 AGACATTATGACAAAGGTGTGTTCTTGGGTACAGCGGCTCTCTCGCGGCATTGGAAG 1862  
 793 gileArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 813  
 1863 AATTGCGAGCTTTAGCCCTCTCAAGAGAGCCCTTGACCATCCAGGTCTTTACTGTGGCAA 1922  
 813 nAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAs 833  
 1923 TGCCCTTCGACCTTAATTAATACACCTTCTGTAAGAAGAAGAGAAATCTTTCAA 1982  
 833 nAlaIleProThrPheSerAlaTyrValIleGluGluTyrGlyGluCysSerLysSerCy 853  
 1983 TGCTATCCCACTTTTTCAGCATGGTCAATGAAGAGTGGGCGAATGTCTTAAGTCATG 2042  
 853 sGluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAla 873  
 2043 TGAATGGTGTGGCAGAGAGACTGTGTAATGCCGAGACATTAATGGACGCTGCTTC 2102  
 873 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 893  
 2103 CGAGTGTGCAAGGAAGTGAAGCCAGCCAGCCAGACCTTTGTGCAGACCATCCCTGCC 2162  
 893 oGlnTyrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLysLy 913  
 2163 CCAGTGGCAGCTGGGGAGTGGTCAATGTCTTAAGACCTGTGGGAAGGGTTACAAAA 2222  
 913 sArgSerLeuLysCysLeuSerHisAspGlyValLeuSerHisGluSerCysAspPr 933  
 2223 AAGAGCTTGAAGTGTCTGTCCATGTGGAGGGGTGTATCTCATGAGAGCTGTGATCC 2282  
 933 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950  
 2283 TTTAAGAAACCTAAACATTTTCATAGACTTTTGACAAATGGCAGAAATGCAGT 2334

## RESULT 5

US-09-445-023A-2  
 ; Sequence 2, Application US/09445023A  
 ; Patent No. 6563858  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hirose, Kunitaka  
 ; APPLICANT: Inoguchi, Biiji  
 ; APPLICANT: Hakozaki, Michinori  
 ; APPLICANT: Ishioka, Keiko  
 ; APPLICANT: Ishida, Yukako  
 ; APPLICANT: Matsushima, Kouji  
 ; APPLICANT: Kuno, Kouji  
 ; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical  
 ; FILE REFERENCE: Q57092  
 ; CURRENT APPLICATION NUMBER: US/09/445,023A  
 ; PRIOR FILING DATE: 1999-12-03  
 ; PRIOR APPLICATION NUMBER: JP 9-160422  
 ; PRIOR FILING DATE: 1997-06-03  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 2184  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: (1)..(2184)  
 US-09-445-023A-2

Alignment Scores:  
 Pred. No.: 0 Length: 2184  
 Score: 3947.00 Matches: 712  
 Percent Similarity: 99.44% Conservative: 4  
 Best Local Similarity: 98.89% Mismatches: 4  
 Query Match: 76.06% Indels: 0  
 Gaps: 4  
 DB:





Db 1561 TCCAGAAACATATGCGAGCTTTCTGGCTATTAGAGCCGCTGATGTAACCTATATCTGAAT 1620  
Qy 764 GlyAspIyThrLeuSerThrLeuGluAspIleMetTyrLysGlyValValLeuArg 783  
Db 1621 GGAACACTTCTCTGTCCAGACTAGACAGACCTTCACTACAAAGAGTACTGCTTAAAG 1680  
Qy 784 TyrSerGlySerSerAlaLeuLeuGluArgIleArgSerPheSerProLeuLysGluPro 803  
Db 1681 TACAGTGGTTCCTCGGCTGGCTGGAAGAATCCGAGCTTTAGTCCACTCAAGAACCC 1740  
Qy 804 LeuThrIleGlnValLeuThrValGlyValAsnAlaLeuArgProLysIleLysTyrThrTyr 823  
Db 1741 TTAACCAATCCAGGTTCTATGTAGGCGATCTCTCCGACCCAAATTAATTCRCCTAC 1800  
Qy 824 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 843  
Db 1801 TTTATGAAGAAGAACAGACAGACTCATTCAGCCATTCGCCATTTCTGAGTGGGTGATT 1860  
Qy 844 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTTPGlnArgArgLeuValGlu 863  
Db 1861 GAAAGTGGGGGAGTGTCTCAAGACATTCGGCTCAGGCTGGCAGAGAGTAGTGCAG 1920  
Qy 864 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 883  
Db 1921 TGCAGAGACATTAACGACACCTCTTCCGAATGTGCAAGGAAGTGAAGCCAGCCAGT 1980  
Qy 884 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 903  
Db 1981 ACCAGACCTTGTGCAGACCTTCTCTTGCCACACTGGCAGTGGGGGATTTGGTCAACCAT 2040  
Qy 904 SerLysThrCysGlyLysGlyTyrLysLysArgSerLysLysCysLeuSerHisAspGly 923  
Db 2041 TCCAAACTTCGGGAAGGTTTACAGAGAGAACCTTGAAATGTGTGTCCTCCACGATGGG 2100  
Qy 924 GlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPheIleAspPhe 943  
Db 2101 GGCCTGTATCAATAGAGCTGTGATCTCTTTGAAGAAGCCAAAGCATTTACATTGACTTT 2160  
Qy 944 CysThrMetAlaGluCysSer 950  
Db 2161 TGCACATGACACAGTGCAGT 2181

RESULT 7

US-09-369-364A-8  
; Sequence 8, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurskainen, Tiina L.  
; APPLICANT: Hirshata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 3638  
; TYPE: DNA  
; ORGANISM: Mus musculus ADAMTS-8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (278)..(2952)  
; NAME/KEY: misc feature  
; LOCATION: (3636)  
; OTHER INFORMATION: n = T  
US-09-369-364A-8  
Alignment Scores:  
Pred. No.: 8,44e-201 Length: 3638  
Score: 2284.50 Matches: 449  
Percent Similarity: 63.10% Conservative: 146  
Best Local Similarity: 47.61% Mismatches: 265

Query Match: 44.03% Indels: 83  
DB: 4 Gaps: 21  
US-09-373-658C-2 (1-950) x US-09-369-364A-8 (1-3638)  
Qy 17 ProThrLeuLeuLeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgPro 36  
Db 308 CCGCCCTCTCTGTCTGCTATTTCAGCTGCGCGCCGCCACTCTCTCTCGCGAGCCCG 367  
Qy 37 Ser-----GluGluAspGluGluLeuValValProGluLeuGluArgAla 51  
Db 368 GCGGGCGCGGACCGCGGCGCGCTCGGAGCTAGTGTGCTCC-----ACGCGGTG 421  
Qy 52 ProGlyHisGlyThr---ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeu 70  
Db 422 CCGCGCAGCGCGAGCAGCGAGCTCGCTTCACCTGTCCGCTTCGCGCAGGCGCTTCGTGCTG 481  
Qy 71 GluLeuArgProAspSerSerPheLeuAlaProGlyPheThrLeuLeuAsnValGlyArg 90  
Db 482 CGCTCGCGCTGTCGCCAGCTTCTTGGCGCCCGAATTCAAGATCGAGCGCTCGGGGGC 541  
Qy 91 LysSerGlySerGluTrpProLeuProGluThrAspLeuAlaHisCysPheTyrSerGly 110  
Db 542 TCGAGCGCGCGCGCGG-----GGCGAGCGCGGACTGCGTGGCTCTCTCTCTCTGCG 595  
Qy 111 ThrValAsnGlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGly 130  
Db 596 ACAGTGAATGGAACCGGAGTCTGCGCGCGCATGAGCTGTGTCGCGGCTCGAGCGCGC 655  
Qy 131 AlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer----- 148  
Db 656 TCGTCTCTGCGCAGCGCGAGGATTCACATCCAGCCACAGGGCGCTGGGACTCCCTG 715  
Qy 149 -----GluArgLeuAlaThrAlaAlaProGlyGluLysPro----- 160  
Db 716 GACACGCTCATCGCTGCAGCGCTGGGGCGCGGACAGCGCGCGCAAGACCCCGGGCTC 775  
Qy 161 -----ProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172  
Db 776 GCTCGCGCGCGAAGCTTTTCCCTCCCTCAAGGACTCGAGTGGGAGGTGGAGATGGGTAAT 835  
Qy 173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192  
Db 836 GCGCAGGAGCAG----- 847  
Qy 193 LysAlaGluThrGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212  
Db 848 -----GAGAGAGTGCACACGAGAGAGGACAGACGAGCAGGAGGGGTGCTCAA 901  
Qy 213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232  
Db 902 GAGACAGAGACTCC-----CGCAAAGTCCACACCCCTTCGGATCC---AAAACATGA 952  
Qy 233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252  
Db 953 AGCAGAGGTTTGTCTCCGAGGCTCGCTTCGTGGAACACTTCTGTGCTGATGCTGCTCC 1012  
Qy 253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272  
Db 1013 ATGCTGCTCTTATGGGACCGACCTTCAGAACACATCTCAGCTGATGTCAATGGCA 1072  
Qy 273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIle 292  
Db 1073 GCCCGAATCTACAAGCACCAGCAGCATCAGGAATCTCGTCAACCTTGTGGTGGTGAAGTG 1132  
Qy 293 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu 312  
Db 1133 CTAAATAGTGAAGAAAGAGATGGGCGCGGAGTGTCCGACACCGGGGGGCTCACACTG 1192  
Qy 313 ArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 332  
Db 1193 CGCAACTTCTGACGTGGCAACGGCGCTTTTCAACAGCCCGAGTGCACCGCCAGCGAC 1952



333 TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGly---SerGlnThrCysAsp 351  
1253 TATGACACTGCCATCTTTTCCACGACGAGACTTCTGTGGAGGAGGAGGAGTGTGAC 1312  
352 ThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIle 371  
1313 ACCCTGGGATGCGACAGCTGTGCACCATCTGTGACCCCGACAGAGAGCTGTCTGATGTC 1372  
372 GluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsn 391  
1373 AAGGATGAGGAGCTGAGGAGGAGCTACACCTGTGGCCCATGAGTGTGAGGAGCTGTCTGAGC 1432  
392 MetProHisAspAspAlaValGlnCysAlaSerLeuAsnGlyValAlaAsnGlnAspSerHis 411  
1433 ATGCCCATGATGATTAAGCCCTGTGTGAGATTTGTTGGGCCCATGAGGAGTGTCTGAGTACCAC 1492  
412 MetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAla 431  
1493 ATGATGGCCCATTTCTTTCATCCAGCGAAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1552  
432 TyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGln 451  
1553 GNTACCTCACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1612  
452 AsnProIleGlnLeuProGlyAspLeuProGly-----ThrSerTrpAspAlaAsnArg 469  
1613 TCGGTTCTGCCCTCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1672  
470 GlnCysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAla-----Ser 487  
1673 CAGTGCAGCAGATCTTGGGCTGATTTCCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1732  
488 ThrCysSerThrLeuTrpCysThrGlyThrSerGlyValValLeuValCysGlnThrLys 507  
1733 ATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1792  
508 His-----PheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsn 525  
1793 AATGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1852  
526 GlyLysCysValAsnLysThrAspArgLysHisPheAspThrProPheHisGlySerTrp 545  
1853 GGTAGCTGTGTACTCAAGGAGGATGTGGAGATCCCAAGGCTGTGTAGTGTGAGTGTGAGTGTGAG 1912  
546 GlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGlnThrThr 565  
1913 GGTCTCTGGAGACCTCGGGGACAAATGTTCTCGACACTGTGTGTGGAGGATACAAATCTCG 1972  
566 MetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGlyLysArg 585  
1973 AACCTGTGATGTGATTAATCCATGCTCAGATGTGAGGAGAGATTTTGTCTGGGTGAAAGA 2032  
586 ValArgTrpArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArg 605  
2033 GTCAAGTACCAATCATGCAACACAGAGGAATGCCACCA--AACGGAAGAGCTTCCGG 2089  
606 GluGlnGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAla 625  
2090 GAGCAGAGTGTGAGAAAT 2146  
626 ValGluTrpIleProLysTrpAlaGlyValSerProLysAspArgCysLysLeuIleCys 645  
2147 CTGCACTGGGTCCTCCCAAGTATTTCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2206  
646 GlnAlaLysGlyIleGlyTrpPhePheValLeuGlnProLysValValAspGlyThrPro 665  
2207 AGAGCCCTGTGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2266  
666 CysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGlyCysAsp 685  
2267 TGTGACCGGATACTCTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2326  
686 ArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySer 705

2327 CATGTGGTGAATCACTACCTAAGAGCTGACAAATGTGGGGTGTGTGGGGGCAAAAGGCATC 2386  
706 ThrCysLys 725  
2387 GCTGTAGAGAGATCTCGGTTCTTTTCAACCCCTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 2446  
726 ThrIleProTrpGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArg 745  
2447 ACCATCCAGCTGTGGTGCACAAACATTGATGTGAACAGGAGGATCCACCCAGGGTTCAGG 2506  
746 AsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTrpIleLeuAsnGlyAsp 765  
2507 AACGACGCGAGCTACCTGCGCTGAAGACAGCAATATGGGAGTCTGCTGCTCAATGGTAAAC 2566  
766 TyrThrLeuSerThrLeuGluGlnAspIleLysLysLysLysLysLysLysLysLysLysLysLys 785  
2567 CTGGCATCTCTGCCATAGACAGACATCTGTGAAGGGGACCATCTGAGGTACAGT 2626  
786 GlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThr 805  
2627 GGTCCATGCTACCTCGAGCGGCTGCAGAGCTTCCAGGCCCTGCTGAGCCTCTTACA 2686  
806 IleGlnValLeuThrVal---GlyAsnAlaLeuArgProLysIleLysTrpThrTrpPhe 824  
2687 GTACAGCTCTGACTGT 2746  
825 Val-----LysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 834  
2747 GTTCCCATGACATGGACTTCAGGCTGAGATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2806  
835 IleProThrPhe-----SerAlaTrpValIleGluGluTrpGlyGluCysSerLysSer 852  
2807 ATTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2866  
853 CysGluLeuGlyTrpGlnArgLeuValGluCysArgAspIleAsnGlyGlnProAla 872  
2867 TCCAGAGTACTGGCAGCGGAGCTGTGAAATGCAAGGACCCCTCAGGTACAGCCTCT 2926  
873 SerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892  
2927 GACACCTGTGATGAGGCTCTGAAACCTGAGGATGCCAAGCCCTGTGGAAGCAGCGGTGT 2986  
893 Pro-----GlnTrp-----GlnLeuGlyGluTrpSerSer 902  
2987 CCCTCTGATCCCTTGTGGAATCTTTAGGCTTATGGAATTTGGGCTACTGG----- 3040  
903 CysSerLys 905  
3041 TGTAAACAGA 3049  
RESULT 8  
US-09-392-184-7/c  
; Sequence 7, Application US/09392184  
; Patent No. 6395889  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN  
; TITLE OF INVENTION: PROTEASE HOMOLOGS  
; FILE REFERENCE: 5800-55  
; CURRENT APPLICATION NUMBER: US/09/392,184  
; CURRENT FILING DATE: 1999-09-09  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 3126  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)\_(3126)  
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)  
US-09-392-184-7

## Alignment Scores:

Pred. No.: 6,428-191 Length: 3126  
 Score: 2176.50 Matches: 445  
 Percent Similarity: 62.46% Conservativity: 139  
 Best Local Similarity: 47.59% Mismatches: 243  
 Query Match: 41.94% Indels: 110  
 DB: 4 Gaps: 23

US-09-373-658c-2 (1-950) x US-09-392-184-7 (1-3126)

Qy 59 LeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPhe 78  
 Db 3116 CTCACCTGTCCGCTTCGGCAAGGCTTCGTCGCTGGCTGGCGCCGACGACAGCTTC 3057  
 Qy 79 LeuAlaProGlyPheThrLeuGlnAsnVal-----GlyArgLysSerClySerGlu 95  
 Db 3056 CTGGCGCCGACTTCAAGATCAGCGCTTCGGGGGCTCCGGCGCGGCGACCGGGGCGC--- 3000  
 Qy 96 ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp 115  
 Db 2999 -----GAGCGGGGCTGGCGGCTGCTTCTTCGGCACCGTCACGGGTC 2952  
 Qy 116 ProSerSerAlaAlaLeuSerLeuGlyGlyValArgGlyAlaPheTyrIleuLeu 135  
 Db 2951 GCCGAGTCGCTGGCGCGCTGAGCTGTGCCGCGGCTGAGCGGCTCTCTCTGCTGGAC 2892  
 Qy 136 GlyGluAlaTyrPheIleGlnProLeuProAlaAlaLaser-----GluArg 150  
 Db 2831 GCGGAGGAGTTCACATCCAGCGCGAGCGCGGGGGCTCTCTGGTTCAGCGCGACCGC 2832  
 Qy 151 LeuAlaThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArg 170  
 Db 2831 CTGACGCGCTGGGGTTCGCGC-CGAGCGCGCGCGCTCC-----GCG 2791  
 Qy 171 ArgAsnArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgPro 190  
 Db 2790 AGGACCGAGTGGGAGTGGAGCGGAGA---GGTTCAGAGCGAGGAGGAGGAGACCA 2734  
 Qy 191 ThrGly-LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyPr 210  
 Db 2733 CCAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2674  
 Qy 210 oGlnTrpSerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyLys 230  
 Db 2673 A-----CCGCGCTTCGGGGCGCCACGAG 2653  
 Qy 230 rIleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAs 250  
 Db 2652 T---AGGACCAAGCGTGTGTCTGAGCGCGCTTCGTGGAGACGCTGCTGTGGCGGA 2596  
 Qy 250 pGlnSerMetAlaGluPheHisGlySerGlyLysHisTyrIleuLeuThrLeuPheSe 270  
 Db 2595 TGCGTCCATGCTGCTCTACGGGGCGGACCTCAGAACCCACACATCTCTGAGCTTAATGTC 2536  
 Qy 270 rValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVa 290  
 Db 2535 TGTGGACCGCGATCTACAGCACCACCGAGATCAAGATTCATCAACCTGATGTGGT 2476  
 Qy 290 lIysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLe 310  
 Db 2475 AAAAGTGTGATGTAGAAATGAAATGGGGCCAGAGGTGTCGCAATGGGGGCT 2416  
 Qy 310 uThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAl 330  
 Db 2415 TACACTGGTAACCTCTGCACTGGCAGCGCGTTCACCGCCCGGCGACCGCCACCC 2356  
 Qy 330 aGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuGlySerGln---Th 349  
 Db 2355 AGAGCACTACGACCGGCTCTCTGCTCACCAGACAGAACTTCTGTGGGAGGAGGGGCT 2296  
 Qy 349 rCysAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSe 369  
 Db 1284 GTGTGTGGGGGCAAGGCAACTCTCTCGAGGAAGGTCTCTCGGGGTCTCTACCCCAACCAAT 1225

Db 2295 GTGTGACACCTGGTGTGGCAGACATCGGAGCAATTTGTGACCCCAACAAAGCTGCT 2236  
 Qy 369 rValIleGluAspAspGlyLeuGlnAlaPheThrThrAlaHisGluLeuGlyHisVa 389  
 Db 2235 CGTGATCGAGATGAGGGGTTCAGGGCGGCCACACCTCGCCCTGAACCTAGGACAGT 2176  
 Qy 389 lPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAs 409  
 Db 2175 CTGAGCATGCCCCACGACGACTCCAAGCCCTGCACACGGCTCTTCGGGGCCATGGGCAA 2116  
 Qy 409 pSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCy 429  
 Db 2115 GCACCATGTATGTCACCGCTGTTCGTCACCTGAACACGACGCTGCCCTGGTCCCCCTG 2056  
 Qy 429 sSerAlaTyrMetIleThrSerPheLeuAspAsnGlyHis-----G1 443  
 Db 2055 CAGCGCATGTATCTCAGAGAGCTTCTTGACGGGGGCGACCGATTTTCAGGTATTTATGGC 1996  
 Qy 443 YGluCysLeu-MetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyT 463  
 Db 1995 CCTGTGTCTAGGTG----- 1982  
 Qy 463 hrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysP 483  
 Db 1981 -----CTACAGCGTTCATATGCTCTTTGGGCGCGATTTCCGCCACTGCC 1936  
 Qy 483 roAsp-----AlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGly 501  
 Db 1935 CCACACCTCTGTCAGGACGCTCTGCGCCCGAGTTTGTGTC-----CACACTGATGGGCTG 1879  
 Qy 501 allLeuValCysGlnThrLysHis-----PheProTrpAlaAspGlyThrSerCysGlyG 519  
 Db 1878 AGCCCTGTGCCACACCAAGATGGCAGCTGCTGCGCGCGTGCACGCGCGCTGCGGGC 1819  
 Qy 519 LuGlyLysTrpCysIleAsnGlyLys-CysValAsnLysThrAspArgLysHisPheAsp 538  
 Db 1818 CTGGCGACCTCTCTCAGAGGCGAGCTGCTACCTGAGGAGGAGTGGAGAGGCCCAAG 1759  
 Qy 539 ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCys 558  
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 Qy 599 AsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAla 618  
 Db 1578 ---GACCGGAAAAAGCTTCAGGGAGCAGCTGTGAGAAATATAATCTTACAAATTACACT 1522  
 Qy 619 SerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLys 638  
 Db 1521 GACATG---GACGGGATCTCTGTCAGTGGTCCCCCAAGTATGCTGGGGTGTCCCCCGG 1465  
 Qy 639 AspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnPro 658  
 Db 1464 GACCGTGAAGTGTGTCTGCGGAGCGCGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1405  
 Qy 659 LysValValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGln 678  
 Db 1404 AGGTGATTTGATGGCACCTCTGTGTGGGCCAGAAAGCTGGCCATCTGTGTCTGCGGCGAG 1345  
 Qy 679 CysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGly 698  
 Db 1344 TGTGTCAAGCGCGCTGTGACCATGTGTGTGACTCCCTCGGAGGTGAGCAAAATCGCGG 1285  
 Qy 699 ValCysGlyGlyAsnGlySerThrCysLysLysLysLysSerGlySerValThrSerAlaLys 718  
 Db 1284 GTGTGTGGGGGCAAGGCAACTCTCTCGAGGAAGGTCTCTCGGGGTCTCTACCCCAACCAAT 1225



D	1213	GTGATCTCTGGGTCAGGCGAGAGGGGGCCCCAAGTGGGGGCCAAGTGTGTCGCCACGACCTG	12172
Q	313	ArgAsnPhcCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis	332
D	1273	CGCAGCTTCTGTGCTGCAGCGGGGCGCTCAACACCCCTGAGGACTCGGACCCCTGACCAC	1332
Q	333	TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr	352
D	1333	TTTGACACAGCCATCTCTGTTTACCGGTGAGCACTGTGTGGAGTCTCCACTTGGCAGACG	1392
Q	353	LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu	372
D	1393	CTGGGTATGGCTGATGTGGGCACCGTCTGTGACCGCGCTCGGACTGTGCCATTGTGGAG	1452
Q	373	AspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMet	392
D	1453	GATGATGGCTCCAGTCAAGCTTCACTGCTCTCATGAATGGGTCTATGCTTTCAACATG	1512
Q	393	ProHisAspAlaLysGlnCysAlaSerLeuAsnGly--ValAsnGlnAspSerHis	411
D	1513	CTCCATGACAACTTCAGGCCATGATCAGTTTGATGGGCTTTGAGCACTCTCGCCAT	1572
Q	412	MetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAla	431
D	1573	GTCAATGGCCCTGTGTGATGGGTCAATGTGGATCTCTGAGGAGCCCTGGTCCCCCTGCAGTGC	1632
Q	432	TyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGln	451
D	1633	CGCTTCATCACTGACTTCTCTGGACAATGGCTATGGGCACCTGTCTCTTAGACAACACAGAG	1692
Q	452	AsnProIleGlnLeuProGlyAspLeuProGlyThrSerTrpAspAlaAsnArgGlnCys	471
D	1693	GCTCCATTGCACTGCTGTGACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGC	1752
Q	472	GlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThr	491
D	1753	CAGCTGACCTTGGGCCCCGACTACGCCAATGTCTCCAGCTGCGCGCGCCCTGTGTGCC	1812
Q	492	LeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrp	511
D	1813	CTCTGTGTCTTGGCCACTCAATATCCACAGGCTGTGGGTCCTTCTGGGACCATGG	1872
Q	512	AlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLys	531
D	1873	GCCGATGGCACACCTTCGGGCGCCGACAGCCCTGCATGGGTGTGTGCTGCTCCACATG	1932
Q	532	ThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrp	551
D	1933	GACCAGCTCCAGGACTTCATATATCCACAGGCTGTGGGTCCTTCTGGGACCATGG	1992
Q	552	GlyAspCysSerArgThrCysGlyGlyValGlnTrpThrMetArgGluCysAspAsn	571
D	1993	GGTGACTGTCTCGGACCTGTGGGGGTGGTGTCCAGTTCTCTCCCGACACTGCACGGG	2052
Q	572	ProValProLysAsnGlyLysTrpCysGlyGlyLysArgValArgTrpArgSerCys	591
D	2053	CCGTCCCCGGAAATGATGGCAAGTACTGTGAGGGCGCGGTACCCGCTTCGCGTCTCTGC	2112
Q	592	AsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAla	611
D	2113	AACACTGAGGACTGCCCACTGCTCAGCCCTCAGCCTTCGCGAGGAGCAGTGTGCTGCC	2172
Q	612	HisAsnGluPheSerLysAlaSerPheGlySerGlyProAla---ValGluTrpIlePro	630
D	2173	TACAACACCGCACCGACCTC---TTTCAAGAGCTTCCAGGGGCCCATGAGACTGGGTCTCT	2229
Q	631	LysTrpAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle	650
D	2230	CGCTACACAGCGCTGGCCCCCAGAGACCATGTCCAAACTCACCTGCCAGGCCCGGGCACTG	2289
Q	651	GlyTrpPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer	670
D	2290	GGTACTACTATGTGTGGAGCCACGGGTGTGTAGTGGGACCCCTGTGTCCCGACAGC	2349

RESIST 10

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RESOLV 10
US-09-634-286A-1
? Sequence 1, Application US/09634286A
? Patent No. 6521436
? GENERAL INFORMATION:
? APPLICANT: Bristol-Myers Squibb Company
? TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
? FILE REFERENCES: DM6909A
? CURRENT APPLICATION NUMBER: US/09/634,286A
? CURRENT FILING DATE: 2000-08-09
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: Patent version 3.0
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Qy 216 pProAlaLeuGlnGlyValGlyGlnProThrGlyThr-----ClySerIle 231  
Db 832 CTCTTGACCACTCCGCTCTCTCCCGCGCTGGGGGCTCAGACCGCAGACGCTGGTGGCGG 891  
Qy 231 eArgLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspG1 251  
Db 892 -CGCGGCGCGCTCCATCTCCCGGCGCGCGAGTGGAGCTCTCTGCTGCTGACGC 950  
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Qy 271 lAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVally 291  
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Qy 291 sIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuth 311  
Db 1071 GGTGGTGGTCTAGCGCACAGCAAGAGCCCTGGAAGTGAAGCAAGACGCTGCCACAC 1130  
Qy 311 rLeuAArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGl 331  
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Qy 351 pThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIle 371  
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Qy 511 pAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLy 531  
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Qy 671 rSerValCysValGlnGlyCysValLysAlaGlyCysAspArgIleIleAspSerLy 691  
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Qy 711 rGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAl 731  
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Db 2385 AACCCACATAAAGTTTCGACAGTTCAAAGCCAAAGACACAGACTAGATTCACTGCCTATT 2444  
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Qy 809 uThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLysLy 828  
Db 2625 TGCAACAGACCCCACTAAACCAATTAGATGTGCGTTATAGCTTTTGTTCACAGAGTC 2684  
Qy 828 sLysGluSerPheAsnAlaIleProThrPheSerAla----- 840  
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Qy 841 -----TrpValIleGluGluTrpGlyLysSerLysSerCysGluLeuGlyTr 857  
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RESULT 12
US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-634-286A-14

Alignment Scores:
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Score:          1931.00       Matches:     395
Percent Similarity: 54.23%    Conservative: 124
Best Local Similarity: 41.32% Mismatches:     316
Query Match:      37.21%     Indels:       122
DB:               4         Gaps:        17

US-09-373-658C-2 {1-950} x US-09-634-286A-14 (1-3250)

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QY   48 LeuGluArgAlaProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPhe 64
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QY   144 Leu-----ProAlaAlaSerGlu-----
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RESULT 14  
US-09-369-364A-12  
; Sequence 12, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurstainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 5804  
; TYPE: DNA  
; ORGANISM: Homo sapiens ADAMTS-9  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(5648)  
; NAME/KEY: misc.feature  
; LOCATION: (1406)  
; OTHER INFORMATION: n-T  
; NAME/KEY: misc.feature  
; LOCATION: (1563)  
; OTHER INFORMATION: n-T  
US-09-369-364A-12

Alignment Scores:  
Pred. No.: 1,26e-151 Length: 5804  
Score: 1756.50  
Percent Similarity: 50.93%  
Best Local Similarity: 36.11%  
Query Match: 33.85%  
DB: 4  
Gaps: 24

US-09-373-658C-2 (1-950) x US-09-369-364A-12 (1-5804)

Qy 60 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeu 79  
Db 309 CGCTCTCTGCTTGGCCAGAGTTTCTATTAACTCTACCCCAATGCGGATTTATC 368  
Qy 80 AlaProGlyPheThrLeuGlnAenValGlyArgLysSerGlySerGluThrProLeu--- 98  
Db 369 GCTCCACTGTCTACTGTCACTCTCTGGGACGCCCGGGGTGAATCAGACCAAGTTTAT 428  
Qy 99 -----ProGlnThrAspLeuAlaHisCysPheTyr-SerGlyThrValAsnGlyAspPr 116  
Db 429 TCGAGAGAGACGGGAACCTAAGACACTGTTTCTACAAAGAGCTATGTCATACCACTC 488  
Qy 116 oSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuG1 136  
Db 489 CGAGCACACGGCGCTCATGCTCTCTCTCAGGAATG----- 525

Qy 136 yGluAlaTyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaPr 156  
Db 526 -----AACACAAAATAGGCACAGTAAGAC 551  
Qy 156 oGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAs 176  
Db 552 AGAAGAAAACCCAGA-GCAAGAAAATGGGAGAA-----AGGATTAACCTGGCTGTGA 604  
Qy 176 pValGlyGly---ThrCysGlyValValAspAspGluProArgProThrGlyLysAlaG1 195  
Db 605 CGTAGCAGCATTAACACAGCGCTTAGCAACAGAGGCAATTTCTGCTTATGGTAATAGAC 664  
Qy 195 uThrGluAspGluAspGluGlyThrGluGlyGluAspGlyGlyProGlnTrpSerProG1 215  
Db 665 GCACAAACACAGAGAAAAGAGAGACCACAGA----- 695  
Qy 215 nAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysAr 235  
Db 696 -----AGGCAAAACG 706  
Qy 235 gPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaG1 255  
Db 707 TTTTTCCTATCCACAGGTTTGTAGAGTCTTGGTGGGCGACACACAGAAATGGTTTC 766  
Qy 255 uPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLe 275  
Db 767 ATACCATGGAGAAAACCTTCAACACTATATTTAACTTTTAATGTCAATGTAGCCTCTAT 826  
Qy 275 uTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeuValI1 295  
Db 827 CTATAAAGACCCACAGTATTGGAATTTAATTAATATTATTGTGAATTAATTTGAT 886  
Qy 295 eHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPh 315  
Db 887 TCATAATGAACAGGATGGGCTTCCATATCTTTAATGTCTCAGACAACTATAAAACCT 946  
Qy 315 eCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspTh 335  
Db 947 TTGCCAGTGGCAGCATTCGACAGTCCA-----GGTGGATCATCATCATGATAC 994  
Qy 335 xAlaIleLeuPheThrArgGlnAspLeuCys---GlySerGlnThrCysAspThrLeuG1 354  
Db 995 TGCTGTCTCTTAAACAAGACAGGATATCTGCAGAGCTCAGACAAATGTGATACCTTAG 1054  
Qy 354 yMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAs 374  
Db 1055 CTTGGCTGAACCTGGGAACCATTTGTATCCCTATAGAAGCTGTTCTTATTAGTGAAGATAG 1114  
Qy 374 pGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProH 394  
Db 1115 TGGATTGAGTACAGCTTTTACGATCGCCCATGAGCTGGGCCCATGTGTTTAACATGCTCA 1174  
Qy 394 sAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAl 414  
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Qy 414 aSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet11 434  
Db 1232 TCCAACACTGAACCTTCTACACCAACCCCTGGATGTGGTCAAGTGTAGTCGAAAATATAT 1291  
Qy 434 eThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsn---Pr 453  
Db 1292 CACTCAGTTTTTAGACACTGGTTATGGGAGTGTTTGTCTTAAACGAACCTGAATCCAGAAC 1351  
Qy 453 oIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPh 473  
Db 1352 CTACCCCTTGGCTGTCCACTGCCAGGATCTCTTACACAGTGAATTAACATGNGAAT 1411  
Qy 473 eThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTr 493  
Db 1412 GATT-TTGGACACAGGTTCTCAGGTGGCCCA---TATATGATGCAGTGCAGACGGCTCG 1468  
Qy 493 pCysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAlaAs 513

Db 1469 GTGCAATAACGCTCAATGGAGTACACAAAGGCTGCGGACCTCAGCACACACCTTGGCCGA 1528  
Qy 513 pGlyThrSerCysGlyGluClyLysTrpCysIleAsnGlyLysCysValAsnLysThrAs 533  
Db 1529 TGGAGCGGAGTGGAGCCTGGAAAGCACTGCAAGNATGGATTGTGTT 1577  
Qy 533 pArgLysHisPheAspThrProPhe--HisGlySerTrpGlyWetTrpGlyProTrpG 552  
Db 1578 -CCCAAGAAATGGATGTCCTCCGTGACAGATGGATCTGGGAGTGGAGTCCCTTTGG 1636  
Qy 552 yAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnPr 572  
Db 1637 AACCTGCTCCAGAACATGTGGAGGGGCGCATCAACAGCCATTCGAGAGTGCAACAGACC 1696  
Qy 572 oValProLysAsnGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAs 592  
Db 1697 AGAACCAAAAATGTGGAAATACTGTGTAGACGTAGATGAATTAATTAATGCTGCAAA 1756  
Qy 592 nLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHi 612  
Db 1757 CAGGAGCCATGTCTCAACAGAG--CGAGACTTCCGAGATGAACAGTGT--GCTCA 1810  
Qy 612 sAsnGluPheSerLysAlaSerPhe-----GlySerGlyProAlaValGluTrpI 629  
Db 1811 C-----TTTGACGGGAAGCATTTTAACATCAACCGTCTGCTTCCCAATGTGCGTGGT 1864  
Qy 629 eProLysTrpAlaGlyLysSerProLysAspArgCysLysLeuIleCysGlnAlaLysG 649  
Db 1865 CCCTAAATACAGTGAATCTCATGAGGACCGGTGCAAGTGTCTGCGAGTGGCAGG 1924  
Qy 649 yLeuGlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAs 669  
Db 1925 GAACACAGCTTACTATCAGCTTCGAGACAGAGTGTATGATGGAATCTCTTGTGGCCAG 1984  
Qy 669 pSerThrSerValCysValGlnGlyLysValLysAlaGlyCysAspArgGlyIleAs 689  
Db 1985 CACAATGATATCTGTGTGAGGCTTTGCGGCAAGCTGGATGCGATCATGTTTAA 2044  
Qy 689 pSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLy 709  
Db 2045 CTCAAAACCGCGAGAGATAATGCGGGGTTGTGTGCGGATAATCTTTCATGCAAAAC 2104  
Qy 709 sLeuSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProTh 729  
Db 2105 AGTGGCAGNACATTAATACAGTACATATGTTTACAACTACTGGTTCGAAATTCAGC 2164  
Qy 729 rGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySe 749  
Db 2165 TGGTGTACCAATATGATGTGCGCAGCACAGTTTCTCAGGGGAAACAGACGATGACAA 2224  
Qy 749 rPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSe 769  
Db 2225 CTACTTACTTTATCAGCAGTAAGGTGAATTTCTGCTAAATGGAACACTTTGTGTGCAC 2284  
Qy 769 rThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAl 789  
Db 2285 AATGGCCAAAAGGAAATTCGATTCGGAATGCTGTGTAGTAGTACAGTGGTCCGACAC 2344  
Qy 789 aAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValle 809  
Db 2345 TGGCGTGAAGAATAAATCACTCAACAGATCCGATCGACAGAACTTTTGTCTCAGGTTTT 2404  
Qy 809 uThrValGlyAsnAlaLeuArgProLysIleLysTyrThrPheVal-----825  
Db 2405 GTCGTGGGAAAGTTGTACAAACCCGATGATGCGTATTCCTTCAATATTCATTTGAGA 2464  
Qy 825 -----825  
Db 2465 TAAACCTCAGCAGTTTTTACTGGAACAGTCAATGGGCCATGGCAAGCATGCAGTAAACCCCTG 2524  
Qy 826 -----LysLysLys-----LysGluSer-----831

Db 2525 CCAAGGGGAACGGAACCGAAACCTTTGTTGGACAGGGAATCTGATCAGCTTACTGTTTC 2584  
Qy 831 -----831  
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Qy 831 -----831  
Db 2645 CTGTGACCTGAGTGGCAGTGTGCCAGCAGGAGTGAATGTAGTGCCTCCAGTGTGGCTTGG 2704  
Qy 832 -PheAsnAlaIleProThrPheSerAla-----840  
Db 2705 TTACCGCAATTGGACATCTACTGTGCCAAATATAGCAGGCTGGATGGGAACACTGAGA 2764  
Qy 840 -----840  
Db 2765 GCTTGATGATGTTTTCAGCAGCAGCATFCCCAACCAAGCAACCTGAAAAATGCTCAGG 2824  
Qy 841 -----TtpValIleGluGluTrpGlyGluCysSerLysSerCysG 854  
Db 2825 GGAATGTAAACAGCGGTGGCTGGCTGCTATTCTGCTGGACTGAAATGTTCAAAAAGCTGTA 2884  
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Qy 872 aSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCy 892  
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Qy 892 sProGlnTrpGlnLeuGlyLysTrpSerSerCysSerLysThrCysGlyLysGlyTyrLy 912  
Db 3002 TCACAGTGAATAATCTGGAGACTGGTCAGAGTGTCTGGTCACCTGTGGAAAAGGCGATAA 3061  
Qy 912 sLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAs 932  
Db 3062 GCACAGCCAGCTGTGTGTGCTGAGTGAAGATCGA---TTAAATGATGAATGTGTGA 3118  
Qy 932 pProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950  
Db 3119 CCCTGAGACCAAGCCCAATCT--ATGCAGACTTGTTCAGCAGCCGGAATGTGCA 3170

RESULT 15  
US-09-369-364A-14  
; Sequence 14, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurskainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 2625  
; TYPE: DNA  
; ORGANISM: Mus musculus ADAMS-9  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2) (2623)  
US-09-369-364A-14

Alignment Scores:  
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Score: 1611.00 Matches: 340  
Percent Similarity: 55.99% Conservative: 146  
Best Local Similarity: 39.12% Mismatches: 312  
Query Match: 31.05% Indels: 71  
DB: 4 Gaps: 26



US-09-373-658C-2 (1-950) x US-09-369-364A-14 (1-2625)

Qy	120	AlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyr	139
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Qy	140	PheIleGlnProLeuProAlaAlaSerGlnArgLeuAlaThrAlaAlaProGlyGlnLys	159
Db	68	TT CATTTGAACCACTCGAGCTGTGTGATGAGCAA	115
Qy	160	ProProAlaProLeuGlnPheHisLeuLeuArgAlaAsn	175
Db	116	CAAAACAAACCC	166
Qy	176	AspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGlu	195
Db	167	TCCACAGAAAGCATGCTGTGCCCACTCAGAACTCAAAAATAGTCACAGTAAAGA-CAA	225
Qy	196	ThrGluAspGluAspGluGlyThrGluGlyGluAsp	205
Db	226	CGGGAATTCAGATGCCAAACCGAAGAGGAATAGCTCGCTGACGACGTGGCACT	285
Qy	208	GlutylProGlnTyrSerProGlnAspProAlaLeuGln	220
Db	286	GCTAAAGACGGTTTGGCAACAAGAGTCTCTCTGCTATAGCAA--CCAGACAACAA	342
Qy	221	GlyValGlyGlnProThrGlyThr-GlySerIleArgLysLysArgPheValSerSerHi	240
Db	343	CACAAGGGACAG-----ATGGAACCAACAAGAACCAAAACGCTTTCTGTCTACCC	393
Qy	240	sArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerG1	260
Db	394	ACGGTTTGTAGAGGTATGTTGGTGGCTGACCACAGGATGGTTTATACCAACGAGCAA	453
Qy	260	YLeuLysHisTyrLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSe	280
Db	454	CCTTCAACATTATATCTTAACCTTAATGCTCAATGCTAGCTTCTATCTATAAAGACTCAAG	513
Qy	280	rIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys	300
Db	514	TATTGGAAATTAATTAATATGTATGTATGTGAACCTTAGTTGTGATTCATAATGACAGGA	573
Qy	300	sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTyrPginLys	320
Db	574	AGGACCTTACATAAATTCAATGCCACCAACATTAAAGAACTTTTGCACGTGGCAGCA	633
Qy	320	sGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheTh	340
Db	634	CTCAAAAGAAC-----TACTTGGGTGGGATTCAGCACACACACGCCGTTCTGGTCAAC	684
Qy	340	rArgGlnAspLeuCysGlySerGln---ThrCysAspThrLeuGlyMetAlaAspValG1	359
Db	685	AAGGAAGATATCTGCAGAGCTCAGACAAATGTGACACCTTAGTCTTCTGCACTGGG	744
Qy	359	yThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaL	379
Db	745	AACATTTTGGACCCCTACCGAAGCTGTTCATTTAGTGAACAGACAGTGGGTGACACAGC	804
Qy	379	apheThrThAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysG1	399
Db	805	TTTCACATAGCTCACCGAGCTGGGCCATGTGTTTAATATGCCTCACGATGACAGCAATAA	864
Qy	399	nCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAs	419
Db	865	ATGCCAAAGAA--GAAGGAGTTAAGATGCCCGACATGTCTATGCGACCAACACTGAACCT	921
Qy	419	nLeuAspHisSerGlnProTyrSerProCysSerAlaTyrMetIleThrSerPheLeuAs	439
Db	922	CTACACCAACCCCTGGATGTGGTCAAGTGCAGTGGGAATATACATCACTGAGTTCCTAGA	981
Qy	439	pAsnGlyHisGlyGluCysLeuMetAspLysPro---GlnAsnProIleGlnLeuProG1	458
Db	982	CACGTGGTACCGAGAGTGCTTGTGAATGAACCTGCATCCAGGACCTATCCTTGTGCTTC	1041

QY	458	yAspLeuPrpGlyThrSerTyrAspAlaAenAArgInCysGlnPheThrPheGlyGluAs	478
DB	1042	CCAACTCCCGGGCTCTCTACACAGGTGAATAAACCAATGTCACTGATTTTGGGCCAGG	1101
QY	478	pSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSe	498
DB	1102	CTCTCAAGTGTGCCCC---TATATGATGCAGTGCAGAGCGCTCTGGTGCATAATGTGGA	1158
QY	498	rGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGl	518
DB	1159	TGGAGCACACAAAGGCTGCAGACTCAGCACACGCCCTGGCGAGATGGAACCGAGTGTGA	1218
QY	518	yGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAs	538
DB	1219	GCCTGGAAAGCACTGCAAGTTTGGATTGTGT---CCCAAGAAAGATGGA	1266
QY	538	pThrPro---PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgTh	557
DB	1267	GGGCCCTGCAATATGATGATCTCTGGGAGGTGTGGACCACTTTGGGACCTGCTCAAGAAC	1326
QY	557	rCysGlyGlyValGlnTrpThrMetArgGluCysAspAsnProValProLysAsnGl	577
DB	1327	GTGTGGAGGAGGCATCAAAACAGCCATCAGAGAGTGCAACAGACAGAGCCAAAATATGG	1386
QY	577	yGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysPr	597
DB	1387	TGGGAAGTACTGTGTAGGAAGGAGATGAAGTTTCAATCTCTGCAACCGGAGCCCTGCAT	1446
QY	597	oAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLy	617
DB	1447	GAAGCAGAAAG---CGAGACTTCCGAGAGGAGCAGTGT---GCTCAC-----TTTGATGG	1494
QY	617	sAlaSerPhe-----GlySerGlyProAlaValGluTrpIleAspLysTyrAlaGl	634
DB	1495	CAAAACACTTCAACATCAATGCTCTGTGCCACCGGTACGCTGTGTTTCCCTAAGTACAGCGG	1554
QY	634	yValSerProLysAspArgCysLysLeuIleCysGlrAlaLysGlyIleGlyTyrPhePh	654
DB	1555	AATTTTGATGAAGGACCGGTGCAAGTTGTTCTGCAGAGTGGCAGGAAACACACGCTACTA	1614
QY	654	eValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCy	674
DB	1615	CGAGCTCGAGACAGAGTAGTTACCGGAACCCCTTGTGCCCAGGACACAAATAGCATCTG	1674
QY	674	sValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPh	694
DB	1675	TGTCCAAGGCTTTGCGGCAAGCTGATGTATCATATTTTAAACTCAAAGCTCGGAA	1734
QY	694	eAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysLysIleSerGlySerVa	714
DB	1735	AGATAATGTGGATTGTGGTGGAGATAATTTCTCATGCCAAACAGTGGCAGGAACATT	1794
QY	714	lThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyValAlaThrAsnIl	734
DB	1795	TAACTGTCCATTATGTTTACAATAGTTGTTCGNAITTCGGCTGTGCTACCAAGCAT	1854
QY	734	eGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLy	754
DB	1855	TGACGTGCTCAGCACAGCTCTCAGGGAAGTCTCAGGATGACAACTACTAGCTTTATC	1914
QY	754	sAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAs	774
DB	1915	AAACAGTAAAGGTGAATCTCTGCTAAATGGAGACTTTGTGTCTCATGTCCAAAAGGGA	1974
QY	774	pIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIl	794
DB	1975	GGTCCGCTGGGAGCGCGCTCATGTAGTCAGCGGATCGGACAATGTGTGTGAAGACT	2034
QY	794	eArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAl	814
DB	2035	GAACGTGACGGACCGTATCGACGAGAATCTCTCTCAGGTGTGTCCGTGGGAAGCT	2094

Search completed: June 18, 2004, 19:00:01  
Job time : 286.679 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 18, 2004, 18:42:30 ; Search time 931.168 Seconds  
(without alignments)  
4673.735 Million cell updates/sec

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Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5189	100.0	3261	11	US-09-989-687-1	Sequence 1, Appli
3	5189	100.0	4014	15	US-10-113-286-1	Sequence 1, Appli
4	5189	100.0	4676	14	US-10-105-929-1	Sequence 57, Appl
5	5181	99.8	4309	15	US-10-210-120-57	Sequence 192, App
6	5181	99.8	4459	16	US-10-159-563-192	Sequence 308, App
7	5181	99.8	4459	16	US-10-159-563-308	Sequence 17, Appl
8	5181	99.8	4760	10	US-09-971-4299-17	Sequence 125, App
9	5144	99.1	4014	11	US-09-989-687-125	Sequence 26851, A
10	5097.5	98.2	4848	13	US-10-425-114-26851	Sequence 20, Appl
11	4299.5	82.9	4180	11	US-09-373-658-20	Sequence 20, Appl
12	4299.5	82.9	4180	11	US-09-989-687-20	Sequence 1840, App
13	4292	82.7	4878	12	US-10-152-319A-1840	Sequence 170, App
14	4292	82.7	4878	16	US-10-191-803-170	Sequence 2, Appli
15	3947	76.1	2184	9	US-09-445-023A-2	Sequence 2, Appli
16	3947	76.1	2184	15	US-10-097-597-2	Sequence 2, Appli
17	3947	76.1	2184	15	US-10-097-580-2	Sequence 13, Appl
18	3677	70.9	2184	9	US-09-445-023A-13	Sequence 21, Appl
19	3677	70.9	2184	15	US-10-097-597-13	Sequence 21, Appl
20	3677	70.9	2184	15	US-10-097-580-13	Sequence 21, Appl
21	3421	65.9	9248	10	US-09-373-658-21	Sequence 21, Appl
22	3421	65.9	9248	11	US-09-989-687-21	Sequence 1, Appli
23	3328	64.1	3147	9	US-09-803-589-1	Sequence 9, Appli
24	2667	51.4	3145	9	US-09-803-589-3	Sequence 27, Appl
25	2507.5	48.3	2804	16	US-10-093-463-27	Sequence 7, Appli
26	2494	48.1	3446	9	US-09-965-631-7	Sequence 3, Appli
27	2487	47.9	2853	9	US-09-965-631-3	Sequence 1, Appli
28	2483	47.9	2867	13	US-09-741-151-1	Sequence 24, Appl
29	2482.5	47.8	2937	13	US-10-275-107-24	Sequence 32, Appl
30	2465	47.5	2930	17	US-10-311-035-32	Sequence 3, Appli
31	2340	45.1	3008	10	US-09-373-658-3	Sequence 398, App
32	2340	45.1	3008	11	US-09-989-687-3	Sequence 2850, A
33	2340	45.1	3711	17	US-10-283-975A-398	Sequence 1, Appli
34	2339	45.0	3715	13	US-10-425-114-26850	Sequence 1, Appli
35	2284.5	44.0	3638	9	US-09-918-171A-8	Sequence 1, Appli
36	2203.5	42.5	2940	14	US-10-163-316-1	Sequence 31, Appl
37	2196.5	42.3	2469	14	US-10-163-316-3	Sequence 121, App
38	2173	41.9	4307	13	US-10-358-283-31	Sequence 1, Appli
39	2173	41.9	4307	16	US-10-191-997-121	Sequence 316, App
40	2168	41.8	4192	15	US-10-247-685-1	Sequence 316, App
41	2161	41.6	4407	12	US-09-946-374-316	Sequence 351, App
42	2161	41.6	4407	12	US-10-015-395A-316	Sequence 351, App
43	2161	41.6	4407	13	US-10-206-915-351	Sequence 351, App
44	2161	41.6	4407	13	US-10-199-670-351	Sequence 351, App
45	2161	41.6	4407	13	US-10-201-858-351	Sequence 351, App

ALIGNMENTS

RESULT 1  
US-09-373-658-1  
; Sequence 1, Application US/09373658  
; Publication No. US20030092900A1  
; GENERAL INFORMATION:  
; APPLICANT: Iruela-Arispe, Luisa  
; APPLICANT: Hastings, Gregg A.  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Trullis, Stephen H.  
; APPLICANT: Fronwald, James A.  
; APPLICANT: Terrett, Jonathan A.  
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
; FILE REFERENCES: 1488.1070006  
; CURRENT APPLICATION NUMBER: US/09/373,658  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3261  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)-(2853)
; NAME/KEY: UNSURE
; LOCATION: (3095)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3248)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3255)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3261)
; OTHER INFORMATION: May be any nucleic acid
US-09-373-658-1

Alignment Scores:
Pred. No.: 0 Length: 3261
Score: 5189.00 Matches: 950
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1.0 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-373-658-1 (1-3261)

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Db 1 ATGGCGAACCGCGAGCGGGCTCCGGGCTCCGAGCTTTGGGCGCTTACCCACCGCTGCTG 60
Qy 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluAsp 40
Db 51 CTGCTCGCGCGGGCTACTGGCGGTGTCGAGCGACTCGGGCGGCCCTCCGAGGAGAC 120
Qy 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrArgLeuArg 60
Db 121 GAGGAGCTAGTGGTCCGAGCTGGAGCGCGCCCGGACACCGGACCCAGCGCTCCGC 180
Qy 61 LeuHisAlaPheAspGlnLeuAspLeuGlnLeuArgProAspSerPheLeuAla 80
Db 181 CTGACCGCTTTGACCGAGCGCTGGATCTGGAGTGGCGCGCGACAGCGCTTTTGGCG 240
Qy 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db 241 CCCGGCTTCAGCTCCAGAACGTCGGGCGCAATCCGGTCCGAGACCGCGCTCCGAA 300
Qy 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db 301 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGGTGAATGGCGATCCAGCTCGGCTGCC 360
Qy 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db 361 GCCCTCAGCCTTCGAGGGCGTGGCGGCGCTTCTACCTGCTGGGGAGGCGTATTTTC 420
Qy 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db 421 ATCCAGCGCGCTGCCCGCGCGCAGCGAGCGCTCCGCCACCGCGCGCCCGAGAGCGCG 480
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 180
Db 481 CCGGCACACCTACAGTTTCCACTCTCGGGGGAATCGGAGGCGGACGATAGGCGGCGACG 540
Qy 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 541 TGGGGGTGCTGGAGCAGCGACCGCGCGCTGGGAAAGCGGAGACCGAGAGCGAGGAC 600
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db 601 GAAGGAGCTAGGCGCAGGAGGAGGCGCTCAGTGGTCCGCGCAGGACCCGCGCACTGCAA 660
Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
Db 661 GCGGTAGGACACCCACAGGACCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

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721 CGCTATGTGGAAACCATGCTTGTGGCAGACCATGTCATGGCAGAAATTCACGGGAGTGGT 780
261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
781 CTAAGCATTACCTTCTCACGTTGTTTCGTCGGCAGCCAGATTGTACAAACACCCCCAGC 840
281 IleArgAsnSerValSerLeuValValValLysLysLeuValLysLeuValLysLeu 300
841 ATTGCTAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 900
301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
901 GGGCCGGAGTGACCTCCATGCTGCCCTCACCTCGGGAACCTTTGCAACTGGCAGAAG 960
321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaAlaLeuPheThr 340
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361 ValCysAspProSerArgSerCysSerValLysGluAspAspGlyLeuGlnAlaAlaPhe 380
1081 GTGTGTGATCCGAGCAGAAAGCTGCTCGTCATAGAAGATGATGCTTTTACAAGCTGCCTTC 1140
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1141 ACCACAGCCCTGATATTAGCCACGCTGTTTAACTATGCCACATGATGATGTCAGAGCAGTGT 1200
401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
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421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
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1321 GGTTCATGGGAAATGTTTGTATGACAGACGCTCAGAAATCCCATACAGCTCCAGCGGATCTC 1380
461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
1381 CCTGGCAGCTCTGTACGATGCCAACCGGCGAGTGCAGTTTACATTTTGGGAGGAGCTCCAAA 1440
481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
1441 CACTGCCCTGTATGCAGCCAGCACATGTAGCACCTTGTGTGTGTACCGGACCTCTGGTGGG 1500
501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520
1501 GTGCTGTGTGTCAAAACCAACACTTTCGCTGGCGGATGGCACCAGCTGTGGAGAAGGG 1560
521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
1561 AATGTGTATCAACCGCAGGTGTGTGAACAAACACGACAGAAAGCATTTTGATACGCT 1620
541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
1621 TTTTCATGGAAGCTGGGGAATGTGGGGCGCTTGGGAGACTGTTTCGAGAAAGCTGCGGTGA 1680
561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyr 580
1681 GGAGTCCAGTACACGATGAGGAAATGTGAACCCAGTCCCAAGAAATGAGGAGAAATAC 1740
581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsn 600
1741 TGTGAAGGCAACGAGTGGCTACAGATCCTGTAACTTTGAGGACTGTCCAGACATAAT 1800

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QY 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
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 QY 621 GlySerGlyProAlaValGluThrIleProLysTyrAlaGlyValSerProLysAspArg 640  
 DB 1861 GGGAGTGGGCGCTGGGTGAATGGATTCGCAAGTACGCTGGGCTCTCACCAAGGACAGG 1920  
 QY 641 CysLysIleCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnProLysVal 660  
 DB 1921 TGCACCTCATCTGCCAGCCAAAGCATGGTACTTCTTGGTTTGCAGCCAGGTT 1980  
 QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680  
 DB 1981 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040  
 QY 681 LysAlaGlyCysAspArgIleIleAspSerLysLysIlePheAspLysCysGlyValCys 700  
 DB 2041 AAGCTGGTGTGATCGCATCATAGACTCCAAAGAGTTTGAATAATGGTGGTTTC 2100  
 QY 701 GlyLysAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720  
 DB 2101 GGGGGAATGGATCTACTTGTAAAAAATATACAGGATCAGTTACTAGTGCAAAACCTGGA 2160  
 QY 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740  
 DB 2161 TATCATGATATCATCAATTCGAATGGAGGCCACCAACATCGAAGTGAACAGCGGAAC 2220  
 QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760  
 DB 2221 CAGAGGGATCCAGGACCAATGACGCTTCTTGGCCATCAAGCTGCTGATGACATAT 2280  
 QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleValTyrLysGlyVal 780  
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RESULT 2

US-09-989-687-1  
 : Sequence 1, Application US/09989687  
 : Publication No. US20040002449A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Hastings, Gregg A.  
 : APPLICANT: Ruben, Steven M.  
 : TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
 : FILE REFERENCE: 1488.107000D  
 : CURRENT APPLICATION NUMBER: US/09/989,687  
 : CURRENT FILING DATE: 2001-11-21  
 : NUMBER OF SEQ ID NOS: 126  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1  
 : LENGTH: 3261  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
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 : LOCATION: (1)..(2853)  
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 : LOCATION: (3195)  
 : OTHER INFORMATION: n is any nucleic acid  
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 : LOCATION: (3261)  
 : OTHER INFORMATION: n is any nucleic acid  
 : US-09-989-687-1

Alignment Scores:  
 Pred. No.: 0 Length: 3261  
 Score: 5189.00 Matches: 950  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 DB: 11 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-989-687-1 (1-3261)

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Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
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Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
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Qy 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGlyGly 520  
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Qy 521 LysTrpCysIleAsnGlyCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
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Qy 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640  
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Qy 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800  
Db 2341 GTCTTGGGTACAGCGGCTCTCTCGGCAATGGAAAGAAATTCGAGACTTTAGCCCTCTC 2400  
Qy 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820  
Db 2401 AAAGAGCCCTTCAGCCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATAA 2460  
Qy 821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840  
Db 2461 TACACCTATCTTCGTAAGAGAGAAAGAAATCTTCAATGCTATCCCCACTTTTCAGCA 2520  
Qy 841 TrpValIleGluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860  
Db 2521 TGGGTCTATGAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGTGTTGGCAGAGAAGA 2580  
Qy 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysLysGluValLys 880  
Db 2581 CTGTAGTAATGCCGAGACATTAATGGACAGCGCTGCTCCGAGTGTCCAAAGGAAGTGAAG 2640



QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTyr 900  
 Db 2641 CCAGCCAGCAGCAGACCTTGTGAGACCACTCCCTGCCCCAGTGGCGAGCTGGGGAGTGG 2700  
 QY 901 SerSerCysSerIysThrCysGlyIysGlyTyrlsIysArgSerLeuIysCysLeuSer 920  
 Db 2701 TCATCATGTCTTAAGACCTGTGGAGGGGTACAAAAAAGAAAGCTTGAAGTGTCTGTCC 2760  
 QY 921 HisAspGlyGlyValLeuSerHisGlySerCysAspProLeuIysIysProIysHisPhe 940  
 Db 2761 CATGATGGAGGGGTGTAICTATGAGAGCTGTGATCCCTTAAAGAAACCTAACAATTTC 2820  
 QY 941 IleAspPheCysThrMetAlaGluCysSer 950  
 Db 2821 ATAGACTTTTGCACAATGGCAGATGCAGT 2850

## RESULT 3

US-10-115-286-1  
 ; Sequence 1, Application US/10115286  
 ; Publication No. US20030166065A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jonak, Zdenka  
 ; Trulli, Stephen  
 ; Fornwald, James  
 ; Terrett, Jonathan  
 ; Hasting, Gregg  
 ; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Ratner & Prestia  
 ; STREET: Box 980  
 ; CITY: Valley Forge  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/115,286  
 FILING DATE: 04-Apr-2002  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/845,496

FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Prestia, Paul F  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GH-70000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-407-0700  
 TELEFAX: 610-407-0701  
 TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4014 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Alignment Scores:  
 Pred. No.: 0 Length: 4014  
 Score: 5189.00 Matches: 950  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 15 Gaps: 0

US-09-373-658c-2 (1-950) x US-10-115-286-1 (1-4014)  
 QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
 Db 517 ATGGGGAACCGCGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCGCGTACCCACGCTGCTG 576  
 QY 21 LeuLeuAlaAlaLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
 Db 577 CTGCTCGCGCGCGCGCTACTGGCGGTGTCGGACGCACTCGGGCGGCGCTCCGAGGAGAC 636  
 QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60  
 Db 637 GAGGAGCTAGTGTGTGCGGAGCTGAGGCGCGCGCGGACACGGGACCAACCGCGCTCCGC 696  
 QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluArgProAspSerSerPheLeuAla 80  
 Db 697 CTGCACGCGCTTGGACGCGCTGGATCTGGAGCTGCGGCGCGCAGCAGCAGCTTTTGGCG 756  
 QY 81 ProGlyPheThrLeuGlnAsnValGlyArgIysSerGlySerGluThrProLeuProGlu 100  
 Db 757 CCGGCTTTCAGCTCCAGAACGTGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAA 816  
 QY 101 ThrAspLeuAlaHisCysPheTyrlsThrValAsnGlyAspProSerSerAlaAla 120  
 Db 817 ACCGACCTGGCGCACTGTCTTACTCCGGCACCGTAATGGCGATCCCAAGCTCGGCTGCC 876  
 QY 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrlsLeuGlyGluAlaTyrlsPhe 140  
 Db 877 GCCCTCAGCCTCTCGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGTATTTC 936  
 QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysPro 160  
 Db 937 ATCCAGCGCTGCCCGCGCGCAGCGCGCTCCGACCGCGCGCGCGCGCGGAGGAGCGG 996  
 QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180  
 Db 997 CCGGCACCACTACAGTTCACCTCTCTCGCGGGAATCGGCAGGGCGAGCTAGGCGGACG 1056  
 QY 181 CysGlyValValAspAspGluProArgProThrGlyIysAlaGluThrGluAspGluAsp 200  
 Db 1057 TCGGGGTGCTGGACGACGAGCGCGCGCGCTGGGAAAGCGGAGCGAGGAGGAGGAGGAC 1116  
 QY 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220  
 Db 1117 GAAGGACTGAGGGGAGGAGCGAAGGGCTCTAGTGTGTCGCGCAGGAGCCCGGCTGCAA 1176  
 QY 221 GlyValGlyGlnProThrGlyThrGlySerIleArgIysLysArgPheValSerSerHis 240  
 Db 1177 GGCTAGGACAGCGCCACAGGAACCTGGAAGCATAGAAAGAACGATTTGTTCAGTCACTAC 1236  
 QY 241 ArgTyrlsValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260  
 Db 1237 CGCTATGTGGAACCACTGCTTGTGGCAGACGACGATCGATGGCAGAAATTCACCGGAGT 1296  
 QY 261 LeuIysHisTyrlsLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrlsHisProSer 280  
 Db 1297 CTAAGCATTAACCTTCTCAGCTGTGTTTGGTGGCAGCCAGATTTGTACAAACACCCGAGC 1356  
 QY 281 IleArgAsnSerValSerLeuValValIysIleLeuValIleHisAspGluGlnIys 300  
 Db 1357 ATTCGTAAATTCAGTTAGCTGTGTGTGTAAGATCTTGGTTCATCCACGATCAACAGAG 1416  
 QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnIys 320  
 Db 1417 GGGCGGGAAGTGACCTCAATGCTGCGCTACTCTGCGAACTTTTGCATCTGGCAGGAG 1476  
 QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrlsAspThrAlaIleLeuPheThr 340  
 Db 1477 CAGCACAAACCCAGTCAGCGGATGCGAGCACTATGACACAGCAATTTCTTTTCAACC 1536  
 QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
 Db 1537 AGACGAGACTTGTGTGGTCCAGACATGTATCTCTTGGGATGGCTGATGTTGGAACT 1596

QY 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380  
DB 1597 GTGTGTGTATCCAGCAGAGCTGCTCCGTATAGAGATGATGGTTTACAGCTGCCCTTC 1656  
QY 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCys 400  
DB 1657 ACCACAGCCCATGAATAGGCCACGTGTTAACTATGCCACATGATGATGCAAGCGTGT 1716  
QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
DB 1717 GCCAGCCCTTAATGGTGTGAACCCAGGATTCCTCCACATGATGGGCTCAATCTTCCAACTG 1776  
QY 421 AspHisSerGlnProTrpSerProCysSerAlaTrpMetIleThrSerPheLeuAspAsn 440  
DB 1777 GACCAAGCCCTTGTCTCTCTGCGAGTCCATGATGATGATGATGATGATGATGATGAT 1836  
QY 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
DB 1837 GGTATGGGGAATGTTTATGAGCAAGCTCAGATCCATGATGATGATGATGATGATGATGAT 1896  
QY 461 ProGlyThrSerTrpAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
DB 1897 CTTGGCACCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1956  
QY 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
DB 1957 CACTGCCCTGATGAGCCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2016  
QY 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520  
DB 2017 GTGCTGGTGTGTCAAAACCAACATCTCCCGTGGCGGATGATGATGATGATGATGATGATGAT 2076  
QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
DB 2077 AAATGGTGTATCAACGCAAGTGTGTGACAAACCCAGCAAGATTTTGTATGACCTT 2136  
QY 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
DB 2137 TTTTATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCCAGAAAGTGGGTGGA 2196  
QY 561 GlyValGlnTrpThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrp 580  
DB 2197 GGAGTCCAGTACAGATGAGGATGTGACACCCAGTCCCAAGAAATGGAGGAAGTAC 2256  
QY 581 CysGluGlyLysArgValArgTrpArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
DB 2257 TGTGAGGCAAAACGAGTGGCTACAGATCCTGTAACTTCCAGGACTGTCAGACATAAT 2316  
QY 601 GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
DB 2317 GGAATAACCTTTAGAGAGGAACAAATGTGAAGCACACACAGATTTTCAAAAGCTTCTTT 2376  
QY 621 GlySerGlyProAlaValGluTrpIleProLysTrpAlaGlyValSerProLysAspArg 640  
DB 2377 GGGAGTGGGCTTGGGTGGATGGATTTCCCAAGTACCTGGCTCTCCCAAAAGGACAGG 2436  
QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTrpPhePheValLeuGlnProLysVal 660  
DB 2437 TGAAGCTCATCTGCCAAGCAAGGATGGGTACTTCTCTCTTTTTCAGCCCAAGTT 2496  
QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680  
DB 2497 GTAGATGGTACTCCATGATAGCCAGATTCACCTCTGTGTGTGACAGACAGTGTGTA 2556  
QY 681 LysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCys 700  
DB 2557 AAAGCTGGTGTGATGCCATCATAGACTCCAAAGAAAGTTGATAAATGCTGTGTTC 2616  
QY 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720  
DB 2617 GGGGGAAATGATCTACTTGTAAATAAATATCAGGATCAGTACTACTAGTCAAAACCTGGA 2676

QY 721 TyrHisAspIleIleThrIleProThrGlyValaThrAsnIleGluValLysGlnArgAsn 740  
DB 2677 TATCATGATATCATCAAAATTCCTCACTGGAGCCACCAACATCGAAGTGAAACAGCGAAC 2736  
QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTrp 760  
DB 2737 CAGAGGGATCCAGAAACAATGGCAGCTTCTTCCCATCAAGCTGCTGATGGCACAAT 2796  
QY 761 IleLeuAsnGlyAspTrpThrLeuSerThrLeuGlnAspIleMetTrpLysGlyVal 780  
DB 2797 ATCTTAATGGTGACTACACTTTGTCACCTTAGAGCAAGACATATGTACAAAGGTGT 2856  
QY 781 ValLeuArgTrpSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800  
DB 2857 GTCTTGAAGTACAGCGCTCTCTCGCGCATTGGAAAGAAATTCGCAGCTTTAGCCCTTC 2916  
QY 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820  
DB 2917 AAAGAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAATATAA 2976  
QY 821 TyrThrTrpPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840  
DB 2977 TACACCTACTTCTGTAAGAGAAAGAAAGAAATCTTTCAATGCTATCCCACTTTTCAGCA 3036  
QY 841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860  
DB 3037 TGGGTCAATGAAAGTGGGGCGAATGTTCTAAGTCAATGAAATGGGTGGCGAGAGA 3096  
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880  
DB 3097 CTGGTGAATGCGAGACATTAATGACAGCTTCTTCCAGTGTGCAAGGAAGTGAAG 3156  
QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900  
DB 3157 CCAGCCAGACCCAGACCTTGTGACAGACCATCTCCCTCCCGAGTGGCAGCTGGGGAGTGG 3216  
QY 901 SerSerCysSerLysThrCysGlyLysGlyTrpLysLysArgSerLeuLysCysLeuSer 920  
DB 3217 TCATCATGTTCTTAAGACCTGTGGAGGGTTACAAAGAAAGAGCTTGAAGTGTCTGTCTC 3276  
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940  
DB 3277 CATGATGGAGGGGTGTATCTCATGAGCTGTGATCTTTAAAGAAACCTAAACCATTTTC 3336  
QY 941 IleAspPheCysThrMetAlaGluCysSer 950  
DB 3337 ATAGACTTTTGCACATGCGAATGCACT 3366

## RESULT 4

US-10-105-929-1  
; Sequence 1, Application US/10105929  
; Publication No. US20020137142A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Goodearl, Andrew D.J.  
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
; FILE REFERENCE: 09404/041001  
; CURRENT APPLICATION NUMBER: US/10/105,929  
; PRIOR APPLICATION NUMBER: 2002-03-25  
; PRIOR FILING DATE: EARLIER FILING DATE: 09/130,491  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1998-08-07  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4676  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (450)....(3360)

US-10-105-929-1

## Alignment Scores:

Prec. No.: 0 Length: 4676  
 Score: 5189.00 Matches: 950  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-09-373-658c-2 (1-950) x US-10-105-929-1 (1-4676)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
 Db 511 ATGGGGAACCGCGAGCGGCTCCGGGCTCTGGAGCTTTGGGCGGTACCCAGCTGCTG 570  
 QY 21 LeuLeuAlaAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
 Db 571 CTGCTCCGCGCGCGCTACTGGCCGTGTCCGACGCTCCGGCGCGCTCCCGAGGAGGAC 630  
 QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60  
 Db 631 GAGGAGCTAGTGTGCGGAGCTGGAGCGGCGCCCGGACACGGGACCGAGCTCCGCG 690  
 QY 61 LeuHisAlaPheAspGlnLeuAspLeuGluLeuArgProAspSerPheLeuAla 80  
 Db 691 CTGCAGCGCTTTGACCGAGCGAGTGGATCTGGAGCTCGCGCGCGCGACAGCAGCTTTTGGGG 750  
 QY 81 ProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerGluThrProLeuProGlu 100  
 Db 751 CCGGGCTTCAGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACCGCGCTTCGGGAA 810  
 QY 101 ThrAspLeuAlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAla 120  
 Db 811 ACCGACCTGGCGCACATGCTTACTCCGGCACCGTGGTGAATGGCGATCCCGAGCTCGC 870  
 QY 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPhe 140  
 Db 871 GGCTTCAGCTCTGCGAGGGCGTGGCGCGCTTCTACTCTGCTGGGGAGCGATTTTC 930  
 QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluysPro 160  
 Db 931 ATCCAGCGCTCCCGCGCCAGCGAGCGCTCCGACCGCGCGCGCGCGCGCGGAGGAGCGG 990  
 QY 161 ProAlaProLeuGlnPheHisLeuArgArgAsnArgGlnGlyAspValGlyThr 180  
 Db 991 CCGGCACCACTACAGTTCACCTCTCGCGCGGAAATCGCGAGCGGCGAGCTAGCGCGCAGC 1050  
 QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200  
 Db 1051 TCGGGGTCTGGACGACGAGCGCCCGGCGCTCAGTGGTTCGCGCGCGCGCGCGCGCTGCA 1110  
 QY 201 GluGlyThrGluGlyGluAspGluGlyProGlnProGlnProGlnProAlaLeuGln 220  
 Db 1111 GAAGGAGCTAGCGCGAGGACGAGCGCTCAGTGGTTCGCGCGCGCGCGCGCGCTGCA 1170  
 QY 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240  
 Db 1171 GCGGTAGGACAGCCACAGAGACTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCAC 1230  
 QY 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260  
 Db 1231 CGCTATGTGNAACCATGCTTGTGGCAGACCGAGTCCGATGGCAGATTTCCAGCGAGTGGT 1290  
 QY 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280  
 Db 1291 CTAAAGCATTAACCTTCTACGCTGTGTTTTCGGTGGCGAGCGAGATTGTACAAACACCCCGC 1350  
 QY 281 IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys 300  
 Db 1351 ATTCGTAAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCTCTCCAGATGAACAGAG 1410

QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320  
 Db 1411 GGGCCGGAGTAGCTCCAACTGCTCCCTCTACTCTGGGAACTTTTGCACCTGGCAGAG 1470  
 QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
 Db 1471 CAGCACAAACCCAGTGACCGGATGCAGAGCACTATGACACAGCAATTTCTTTTCCACC 1530  
 QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
 Db 1531 AGACAGGACTTGTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAACT 1590  
 QY 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380  
 Db 1591 GTGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAGATGATGGTTTACAGCTGCTTC 1650  
 QY 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400  
 Db 1651 ACCACAGCCCATGAATTAGGCCACGTTTAAACATGCCACATGATGCAAGAGCTGT 1710  
 QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
 Db 1711 GCCAGCTTAATGGTGTGAACAGGATTTCCACATGATGGGTCAATGCTTTTCCAACTCG 1770  
 QY 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
 Db 1771 GACCAACAGCCAGCTTGTCTCTTGCAGTGCCTACATGATTTACATCTTTCTGCATAAT 1830  
 QY 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
 Db 1831 GGTATGGGGAATGTTTGTATGCAAGCTCAGAAATCCATACACTCCAGGCGATCTC 1890  
 QY 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
 Db 1891 CCTGGCCTCTGTACGATGCCAACCGGCGAGTTCACATTTTACATTTTGGGGAGGACTCCAAA 1950  
 QY 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
 Db 1951 CACTGCCCGGATGAGCCAGCAGCATGTAGCACTTGTGGTGTACCGGCACCTCTGTGGTGG 2010  
 QY 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520  
 Db 2011 GTGTGTGTGTCAAAACCAACACTTCCCGTGGCGGATGTCACAGCTGTGGAGAGGG 2070  
 QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
 Db 2071 AAATGGTGTATCAACCGCAAGTGTGAACAAAAACCGACAGAAAGCATTTTGTATCGCT 2130  
 QY 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
 Db 2131 TTTTCATGGAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCGAGAACCTGGCGGTGA 2190  
 QY 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580  
 Db 2191 GGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGATAC 2250  
 QY 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
 Db 2251 TGTGAAGCAAAACAGTGGCTACAGATCTCTTAACCTTTCAGGAGCTGTCCAGACAAAT 2310  
 QY 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
 Db 2311 GGAATAACCTTTAGAGGAAACAAATGTGAAGACACACACAGAGTTTTCAAAAGCTTCTTT 2370  
 QY 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640  
 Db 2371 GGGAGTCCGGCTCGGTGGAAATGGATTTCCAGTACCTGGCGTCTCCCAAGAGGAGG 2430  
 QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnProLysVal 660  
 Db 2431 TGCAAGTCTATCTGCCAAGCAAAAGGCAATGGTACTTCTTCTGTTTTCGAGCCCAAGTT 2490  
 QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680



947 CTAAGCATTACCTTCACGTTGTTTCGGTGGCAGCCAGATTGTACAAACCCAGC 1006  
281 IleArgAsnSerValSerLeuValValValIleLeuValIleHisAspGluGlnLys 300  
1007 ATTCGTAATTCAGTATAGCTGGTGGTGGTCAAGATCTTGGTCAATCCAGATGAACAGAAG 1066  
301 GlyProGluValThrSerAsnAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320  
1067 GGGCGGAAGTACCTTCCATGCTGCTTCACTTCGCGAATTTTGCAACTGGCAGAAG 1126  
321 GlnHisAsnProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
1127 CAGCAACACCCAGTACCGGATGCGGATGCGAGACATATACACACAGCAATTTTTCACC 1186  
341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGluMetAlaAspValGlyThr 360  
1187 AGACAGGACTTGTGGGTCCACAGATGTGATCTCTTGGATGGCTGTGTTGAACT 1246  
361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaPhe 380  
1247 GTGTGTGATCCGAGCAGAAGTCTCCGTATAGAAAGATGATGTTTCAAGTCCCTTC 1306  
381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCys 400  
1307 ACCACGCCATGAAATTAGCCACGCTGTTTAAATGATGCGCATATGATGCAAGCAGTGT 1366  
401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
1367 GCCAGCTTAATGGTGTGAACAGCAGATTCGCCACATGATGGCGTCAATGCTTCCAACTG 1426  
421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
1427 GACCAAGCCAGCCCTGTGCTCTTCCAGTGGCTATCATGATACATCAATTTCTGGATAAT 1486  
441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
1487 GGTCAATGGGGAATGTTGATGACACAGCTCAGATCCATACACATCCAGGCGATCTC 1546  
461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
1547 CCTGGCACCCTGTAGATGCCAACCGGAGTCCAGTTCATATTTTGGGAGGAGCTCCAAA 1606  
481 HisCysProAspAlaAspThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
1607 CACTGCCCGATGAGCCAGCAGCATGTAGCACCTTGTGTGTACCGGACCTCTGTGGG 1666  
501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGly 520  
1667 GTGCTGGTGTGTCAAAACCAACACATTCCTCGTGGCGGATGGCACCATGTGGAGAAGGG 1726  
521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
1727 AATGTGTATCAACGGCAAGTGTGAACAAACCGACAGAAACATTTTGTATACGCTT 1786  
541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
1787 TTTCATGAAGCTGGGGAATGGGGGCTTGGGGAGACTGTTCAGAACCTGGCGGTGA 1846  
561 GlyValGlnThrThrArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580  
1847 GGAGTCCAGTACACGATGAGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC 1906  
581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
1907 TGTGAAGGCAACGATGGCTGACATCTCTGTAACTTTGAGGACTGTCCAGACATTAAT 1966  
601 GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
1967 GGAAGAACTTTAGAGAGCAATGTGAAGCACACACAGTATTTCAAAAGCTTCCTTT 2026  
621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640

2027 GGGAGTGGGCTCGGTGGAATGGATTCCCAAGTAGCTGGCGTCTCACCAAGGACAGG 2086  
641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660  
2087 TGCAGCTCATCTGCAAGCCAAAGGCATTTGGTACTTCTTCTGTTTTCAGCCAGGTT 2146  
661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680  
2147 GTAGATGCTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGA 2206  
681 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 700  
2207 AAAGCTGTTGTGATCGCATCATAGCTCCAAAGAAAGTTTGTATAAATGTGGTGTTCG 2266  
701 GlyGlyAsnGlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGly 720  
2267 GGGGAATGATCTACTTGTAAAAAATATCAGATCAGTACTAGTGTCAAAACCTGGA 2326  
721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740  
2327 TATCATGATATCATCAAAATTCAACTGGAGCCCAACATCGAAGTGAAGGAGCAAC 2386  
741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760  
2387 CAGAGGGATCCAGAACATGGCAGCTTTCTGCCATCAAGCTGCTGATGGCAGATAT 2446  
761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780  
2447 ATTCTTAATGTGACTACACTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGTGT 2506  
781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800  
2507 GTCCTGAGGTACACGGCTCTCTGCGGCAATGGAAGAATTCGACGCTTTAGGCCCTCTC 2566  
801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysLysLys 820  
2567 AAAGGCCCTTGACCATCCAGTCTTACTGTGGCAATGCCCTTGACCTTAAATTTAA 2626  
821 TyrThrTyrPheValLysLysLysGlySerPheAsnAlaIleProThrPheSerAla 840  
2627 TACACCTACTCTGTAAGAGAGAGAGAGAAATCTTTCAATGCTATCCCCACCTTTTCAGCA 2686  
841 TrpValIleGluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860  
2687 TGGGTCAATGAGAGTGGGGCAATGTCTTAAGTCATGTGANTGGGTGGCAGAGAGA 2746  
861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGlyValLys 880  
2747 CTGTTAGATGCCGAGACATTAATGGACAGCTCTTCCAGTGTGCAAGGAAAGTGAAG 2806  
881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900  
2807 CCAGCCAGCCAGACCTTGTGACAGACATCTCTGCCCTGCCCTGCCCTGGGAGTGG 2866  
901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920  
2867 TCATCATGTTCTAAGACCTGTGGGAAGGTTTACAAAAAGAGAGCTTGAAGTGTCTGTCC 2926  
921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940  
2927 CATGATCGAGGGGTGTATCTCTCATGAGAGCTGTGATCTCTTTAAAGAAACCTTAAACATTT 2986  
941 IleAspPheCysThrMetAlaGluCysSer 950  
2987 ATAGACTTTTGCACATGGCAGAAATGCACT 3016

RESULT 6  
US-10-159-563-192  
; Sequence 192, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus

; APPLICANT: Peterson, Carsten  
 ; APPLICANT: Meltzer, Paul  
 ; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
 ; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
 ; FILE REFERENCE: 11613.56US11  
 ; CURRENT APPLICATION NUMBER: US/10/159,563  
 ; CURRENT FILING DATE: 2002-12-09  
 ; PRIOR APPLICATION NUMBER: US 10/133,937  
 ; PRIOR FILING DATE: 2002-04-25  
 ; NUMBER OF SEQ ID NOS: 444  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 192  
 ; LENGTH: 4459  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-159-563-192

Alignment Scores:  
 Pred. No.: 0 Length: 4459  
 Score: 5181.00 Matches: 949  
 Percent Similarity: 99.89% Conservative: 0  
 Best Local Similarity: 99.89% Mismatches: 1  
 Query Match: 99.85% Indels: 0  
 DB: 16 Gaps: 0

US-09-373-658C-2 (1-950) x US-10-159-563-192 (1-4459)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
 DB 294 ATGGGAAACGGGAGCGGGCTCGGGGCTCGGAGCTTTGGGCGGTACCCACCGCTGGT 353  
 QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
 DB 354 CTGCTCGCGGGGCTACTGCGGTGTGCGAGCACTCGGGGCGCCCTCCGAGGAGAC 413  
 QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60  
 DB 414 GAGGAGCTAGTGGTCCGAGCTGAGCGCGCCCGGACACCGGACCCACCGCTCCGC 473  
 QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerPheLeuAla 80  
 DB 474 CTGACCGCTTTGACGACGCTGATCTGGAGCTGCGGCGCGGAGAGGCTTTTGGCG 533  
 QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100  
 DB 534 CCCGGCTTCAGCTCCAGAGCTGGGGCGCAATCCGGGTCGAGACCGCGCTTCGGAA 593  
 QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValLeuGlyAspProSerSerAlaAla 120  
 DB 594 ACCGACCTGGCGACCTGCTTCTACTCGGACCGGTGAATGGCGATCCAGCTCGGCTGCC 653  
 QY 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140  
 DB 654 GCCCTCAGCCTCTCGAGGGCGTGGCGGCGCCTTCTACCTGCTGGGGAGGCGTATTTC 713  
 QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160  
 DB 714 ATCCAGCGCTGCGCGCGCGCGAGCGGCGCTCCGCCACCGCGCCCGCGGAGAGCG 773  
 QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 180  
 DB 774 CCGGCACCACTACAGTTCACCTCTCTCGCGCGGATCGGCGGCGGAGCTCGGCGGACG 833  
 QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200  
 DB 834 TGGCGGGTCTGGAGCAGCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 893  
 QY 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220  
 DB 894 GAAGGACTGAGGCGAGGAGGAGGAGGCTCAGTGGTGGCGGCGGCGGCGGCGGCGGCT 953  
 QY 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHis 240

DB 954 GGCTAGGACAGCCACAGGAACCTGGAAGCATAAGAAAGAGCGATTGTGTCCAGTCAC 1013  
 QY 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260  
 DB 1014 CGCTATGTGAAACCATGCTTTGGCAGACCACTGATGGCAGAAATCCACGGCAGTGT 1073  
 QY 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280  
 DB 1074 CTAAGCATTTACCTTCTCAGCTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCAGC 1133  
 QY 281 IleArgAsnSerValSerLeuValValValValValValValValValValValValVal 300  
 DB 1134 ATTCTTAATTCAGTTAGCTTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAAG 1193  
 QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320  
 DB 1194 GGGCCGGAAGTGAACCTCAATGTGCTCACTCTGCGGAACCTTTTCAACTGCGAGAAG 1253  
 QY 321 GluHisAsnProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
 DB 1254 CAGCAACACCCACCCAGTGAACCGGATGAGAGACTATGACACAGCAATCTTTTCAAC 1313  
 QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
 DB 1314 AGACAGGACTTGTGGTCCCGACATGTGTACTCTTGGGATGGCTGATGTTGGAACT 1373  
 QY 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380  
 DB 1374 GFTGTGATCCGAGCAGAACTGCTCCGTATAGAAGATGATGGTTTACAAAGCTGCCTTC 1433  
 QY 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400  
 DB 1434 ACCACAGCCCATGANTTAGGCGACGCTGTTTAAATGCCACATGATGATGATGATGATG 1493  
 QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
 DB 1494 GCCAGCTTAAATGTTGAACACAGGATTCACATGATGGCGTCAATGCTTTTCAACCTG 1553  
 QY 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
 DB 1554 GACCACAGCCAGCTTGGCTCTCTTGGAGTGGCTTACATGATGATGATGATGATGATGAT 1613  
 QY 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
 DB 1614 GGTCTATGGGAAATGTTTGTGAGCAAGCTCCAGATCCCATACAGCTCCCGAGCGATCTC 1673  
 QY 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
 DB 1674 CTTGGCAGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1733  
 QY 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500  
 DB 1734 CACTGCCCCGATGACGCGAGCAGCATGTAGCACTTGTGGTGTACCGGACCTCTGGTGG 1793  
 QY 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520  
 DB 1794 GTGCTGTGTGTCAAAACCAACACTTCCGCTGGCGGATGGCAACAGCTGTGGAGAGGG 1853  
 QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
 DB 1854 AATGTGTATCAACGCGCAGTGTGTGAACAAACCCAGACAGAAAGCATTTTGTATGCT 1913  
 QY 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
 DB 1914 TTTTCAGGAGCTGGGGAATGTTGGGGGCTTGGGAGACTGTTTCGAGAACTGCGGTGGA 1973  
 QY 561 GlyValGluTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyr 580  
 DB 1974 GGAGTCCAGTACAGGATGAGGAATGTGAACCCAGTCCCAAGAAATGGAGGAAGTAC 2033  
 QY 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
 DB 2034 TGTGAGGCAACAGAGTGGCTACAGATCCTGTAACTTGGAGACTGTCCACACAATAAT 2093



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QY 601 GlyIysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerIysAlaSerPhe 620
Db 2094 GGAAGAACCTTTAGAGAGGAACAATGTGAAGCACACAGAGATTTTCAAGAGCTTCTCTTT 2153
QY 621 GlySerGlyProAlaValGluTTPileProLysTyrAlaGlyValSerProLysAspArg 640
Db 2154 GGGAGTGGGCGCTGGGTGGATGGATCCCAAGTACGCTGGGCTCTACCAAGGACAG 2213
QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db 2214 TGCAGCTCATCTGCCAAGCAAGGCAATGGCTACTTCTCTGTTTGCAGCCCAAGGTT 2273
QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnCysVal 680
Db 2274 GTAGATGGTACTCCATGTAGCCCGAGATTCACCTCTGTCTGTGTGCAAGACAGTGTGA 2333
QY 681 LysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCys 700
Db 2334 AAGAGCTGGTGTGATCGCATCATAGACTCCAAAGAGAGTTGATAAATGTGTGTTC 2393
QY 701 GlyGlyAsnGlySerThrCysLysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db 2394 GGGGGAATGGATCTACTTGTAAAGAAATATCAGGATCAGTTACTAGTCCAAACCTGGA 2453
QY 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db 2454 TATCATGATATCATCATCAATTCCACTGGAGCCACCAACATCGAGTGAACAGCGGAC 2513
QY 741 GlnArgGlySerArgAsnGlySerPheLeuAlaIleLysAlaIleAspGlyThrTyr 760
Db 2514 CAGAGGGATCCAGGAACAATGGCAGCTTCTTGGCCATCAAGCTGCTGATGSCACATAT 2573
QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db 2574 ATTCTTAAGGTGACTACACTTTGTCCACTTGTACAGCAGACATATATGTACAAAGTGTT 2633
QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db 2634 GTCTTGAGGTACAGCGCTCTCTCGCGCATTCGGAAGAAATTCGACGCTTAGCCCTCTC 2693
QY 801 LysGluProIleThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db 2694 AAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATATAA 2753
QY 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db 2754 TACACCTACTTCTAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 2813
QY 841 TrpValIleGluIleThrGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db 2814 TGGGTCAATTAAGAGGTGGGGCGAATGTTCTAAGTCAATGTAATGGGTTGGCAGAGAAGA 2873
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
Db 2874 CTGGTAGAATCCGAGACATTAATAGACAGCTTCTTCGAGTGTCCAAAGGAGTGAAG 2933
QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db 2934 CCAGCCAGCAGCAGACACTTGTGTGAGACCATCCCTGCCCCAGTGGCAGCTGGGGGAGTGG 2993
QY 901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
Db 2994 TCATCATGTTCTAAGACCTGTGGGAGGGGTACAAAAGAAAGAGCTTGAAGTGTCTGTGCC 3053
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db 3054 CATGATGGAGGGGTATATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAACATTTC 3113
QY 941 IleAspPheCysThrMetAlaGluCysSer 950
Db 3114 ATAGACTTTTGGCAATATGGCAGAAATGCAGT 3143
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## RESULT 7

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US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040609154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308
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## Alignment Scores:

Pred. No.:	0	Length:	4459
Score:	5181.00	Matches:	949
Percent Similarity:	99.89%	Conservative:	0
Best Local Similarity:	99.89%	Mismatches:	1
Query Match:	19.85%	Indels:	0
DB:	16	Gaps:	0

US-09-373-658C-2 (1-950) x US-10-159-563-308 (1-4459)

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QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 294 ATGGGGAACCGGAGCGGCTCCGGGGTCTCGAGCTTTGGGCCCTACCCACGCTCTG 353
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db 354 CTGCTCGCGCGGGCGCTACTGCGCTGCGACGCACTCGGCGCCCTCCGAGGAGGAC 413
QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db 414 GAGGAGCTAGTGTGTCCCGAGCTGAGCGCGCCCGGACACGCGGACACGCGCTCCGC 473
QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
Db 474 CTGCAAGCTTTGACCAAGCAGCTGATCTGGAGCTCGGCGCCGACAGCAGCTTTTGGCG 533
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db 534 CCGCGCTTCACTCCAGAACGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGGA 593
QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db 594 ACCGACCTGGCGCACTGCTTCTACTCCGCGACCGTGAATGGCGATCCCAAGCTCGGCTGCC 653
QY 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db 654 GCGCTCAGCCTCTGCGAGGGGTGCGCGCGCTTCTACTGCTGGGGAGGAGGATTTTC 713
QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db 714 ATCCAGCGCTGCGCGCGCAGGAGCGCTTCCGACCGCGCCCGCCCGGAGGAGGAGCGG 773
QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlnIleAspValGlyGlyThr 180
Db 774 CCGGCAACCTACACTTCCACTCTCTCGCGCGAATCGGACAGCGCGACGCTCGCGCGGACG 833
QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 834 TGCGGGGTCTGTGACGACGAGCGCGCGCGCTGGGNAAGCGGAGCCGAGACGAGGAC 893
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QY	201	Gluc1ThrGluGlyGluAspGluGlyProGlnTrrpSerProGlnAspProAlaLeuGln	220
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QY	221	GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis	240
DB	954	GGCGTAGGACAGCCACAGAACTGGAGAGCTAAGAAAGAGCGATTTGTGTCCAGTCAC	1013
QY	241	AsGlyValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly	260
DB	1014	CGCTATGTGGAAACCAATCTTGTGGAGACCAAGTCGATGGCAGAAATCCACGCGAGTGGT	1073
QY	261	LeuLysHisTyZLeuLeuThrLeuPheSerValAlaIleArgLeuTyLysHisProSer	280
DB	1074	CTAAAGCATTACTCTCACGTTGTTTCGGTGGCAGCCAGATGTACAAACACCCCGCAGC	1133
QY	281	IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys	300
DB	1134	ATTCTGTAATTCAGTTAGCTGTGTGGTGGAGATCTTGGTCTATCCACGATGAACAGAA	1193
QY	301	GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys	320
DB	1194	GGCGCGGAAGTGACCTCCAAATGCTGCCCTCACTCTCGGGAACCTTTTCGAATCGCAGAG	1253
QY	321	GlnHisAsnProProSerAspArgAsnAlaGluHisTyrrAspThrAlaIleLeuPheThr	340
DB	1254	CAGCAACACCCACCCAGTGACCGGATGACAGACACTATGACACAGCAATCTCTTTCA	1313
QY	341	ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr	360
DB	1314	AGACAGGACTTGTGTGGGTCCACACATGTGATCTCTTGGATGGCTGATGTGGAACT	1373
QY	361	ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe	380
DB	1374	GTGTGTGATCCGACGAGAGCTGCTCGGTCTATAGAGATATGCTTTTACAGCTGCCTTC	1433
QY	381	ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys	400
DB	1434	ACCACAGCCCATGAATTAGGCCACGCTGTTTAAACATGCGACATGATGATGCAAGACAGTGT	1493
QY	401	AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu	420
DB	1494	GCCAGCCTTAATGTGTGAACCCAGATCCACATGATGGCGTCAATGCTTTCCAACTGT	1553
QY	421	AspHisSerGlnProTrpSerProCysSerAlaTyrrMetIleThrSerPheLeuAspAsn	440
DB	1554	GACCACAGCCAGCCTTGGTCTCTTCGATGGCCCTACATGATTACATCTTCGGATAAT	1613
QY	441	GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu	460
DB	1614	GGTCATGGGAATTTTGTATGGCAAGCCTCAGAAATCCCATACAGCTCCGACGCGATCTC	1673
QY	461	ProGlyThrSerTyrrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys	480
DB	1674	CCTGGCACTCTGTACGATGTCMAACCGGCGATGGCGATTTTACATTTGGGAGGAGCTCCAA	1733
QY	481	HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly	500
DB	1734	CACTGCCCCGATGCAGCGACACATGTAGCACCTTGTGTGTATCCGGCACTCTGGTGG	1793
QY	501	ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly	520
DB	1794	GTGCTGTGTGTAAACCAACACTTCCCGTGGCGGATGGCACACAGCTGTGGGAAGGG	1853
QY	521	LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro	540
DB	1854	AAATGTGTATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCAATTTTCATACGCT	1913
QY	541	PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly	560
DB	1914	TTTCATGAAGACTGGGGAATGTGGGGCTGTGGGAGACTGTTCAGAAACGTGGCGGTGA	1973

QY	561	GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr	580
DB	1974	GGAGTCCAGTACACCATCAGCGAATGTGCACACCCAGTCCCAAGAATGCAGGAGTAC	2033
QY	581	CysGluGlyLysArgValArgSerCysAsnLeuGluAspCysProAspAsnAsn	600
DB	2034	TGTGAAGGCACAAACGATCGCTACAGATCTCTGTAACTTGAGGACTGTCAGACAATAT	2093
QY	601	GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe	620
DB	2094	CGAAAAACCTTTAGAGAGGAACAATGTGAAGCACACACCAAGTATTTCAAAAGCTTCTCTT	2153
QY	621	GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg	640
DB	2154	GGAGTGGGCTCGCGGTGGAAATGATTTCCCAAGTACGTGGGTCTCACCAAGGACAGG	2213
QY	641	CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal	660
DB	2214	TGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTGTTTTGCAGGCCAAGGTT	2273
QY	661	ValAspGlyThrProCysSerProAsnSerThrSerValCysValGlnGlyGlnCysVal	680
DB	2274	GTAGATGGTACTTCCATGTAGCCCAAGATTCCACTCTGTGTGTGCAGACAGTGTGTA	2333
QY	681	LysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCys	700
DB	2334	AAAGCTGGTGTGATCGCATCATAGACTCCAAAGAAGTTTGATAAATGTGGTGTTC	2393
QY	701	GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly	720
DB	2394	GGGGAAATGGATCTACTCTGTAAAAAAAATATCAGGATCAGTTACTAGTCAAAACCTGGA	2453
QY	721	TyrHisAspIleIleThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsn	740
DB	2454	TATCATATATCATCAAAATTCAACTGGAGCCACCAACATCGAGTGAACACAGCGGAAC	2513
QY	741	GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr	760
DB	2514	CAGAGGGATCCAGGAACAATGGCAGCTTCTTGCCATCAAAAGCTGCTCATGCCACATAT	2573
QY	761	IleLeuAsnGlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrLysGlyVal	780
DB	2574	ATTCCTAATGGTGACTACACTTTGTCCACTTAGACGAAGACATTATGTACAAAGGTGTT	2633
QY	781	ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu	800
DB	2634	GTCTTGAGGTACAGCGCTCTCTGCGGCATTGGAAAGAAATTCGCAGCTTTAGCCCTCTC	2693
QY	801	LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys	820
DB	2694	AAAGAGCCCTTGACCAATCAGGTTCTTACTGTGGGCAATGGCCCTTCGACCTTAAATATA	2753
QY	821	TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla	840
DB	2754	TACACCTACTTCTGAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACCTTTTCAGCA	2813
QY	841	TrpValIleGluTrpGlyGluCysSerLysSerCysGluLeuGlyTyrGlnArgArg	860
DB	2814	TGGGTCAATTGAAGTGGGGCAATGTTCTTAAGTCATGTGAATTTGGGTTGCAGAGAAGA	2873
QY	861	LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys	880
DB	2874	CTGGTAGAATGCGAGACATTAATGACAGCGCTTGTTCCGAGTGTCAAGAAGAAGTAGAAG	2933
QY	881	ProAlaSerThrArgProCysAlaAspHisProCysProGlnTyrGlnLeuGlyGluTrp	900
DB	2934	CCAGCCAGCACACAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGG	2993
QY	901	SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer	920
DB	2994	TCATCATGTCTTAAGACCTGTGGGAAGGGTTACAAAAAAGAAGACTTGAAGTGTCTGTCC	3053
QY	921	HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe	940

Db 3054 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTAAACATTTTC 3113  
Qy 941 IleAspPheCysThrMetAlaGluCysSer 950  
Db 3114 ATAGACTTTTGACAAATGGCAGATGCAGT 3143  
RESULT 8  
US-09-971-429B-17  
; Sequence 17, Application US/09971429B  
; Publication No. US20030175704A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy K. W.  
; APPLICANT: Shvian, Andrew W.  
; APPLICANT: Turner, Christopher M.  
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER  
; FILE REFERENCE: PA-0040 US  
; CURRENT APPLICATION NUMBER: US/09/971.429B  
; CURRENT FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: 60/239,024  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PERL Program  
; SEQ ID NO 17  
; LENGTH: 4760  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 118  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-971-429B-17  
Alignment Scores:  
Pred. No.: 0 Length: 4760  
Score: 5181.00 Matches: 949  
Percent Similarity: 99.89% Conservative: 0  
Best Local Similarity: 99.89% Mismatches: 1  
Query Match: 99.85% Indels: 0  
DB: 10 Gaps: 0  
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Qy 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
Db 612 ATGGGGAAACCGAGACGGGCTCCGGGCTCGGAGCTTTGGGCCAGTACCCACGCTGCTG 671  
Qy 21 leuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
Db 672 CTGCTCGCGCGGCTACTGGCGTGTGGAGCGCACTCGGGCGCCCTCCGAGGAGGAC 731  
Qy 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60  
Db 732 GAGAGCTAGTGTGGCGAGCTGGAGCGCCCGGGAACGGGACACCGCGCTCCGC 791  
Qy 61 leuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProSerSerPheLeuAla 80  
Db 792 CTGCACGCTTTGACGACGCTGATCTGGAGCTGCGCGCGGACAGACGCTTTTGGCG 851  
Qy 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100  
Db 852 CCCGGCTTCAGCTCCAGACAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCGGAA 911  
Qy 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120  
Db 912 ACCGACCTGGGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 971  
Qy 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrThrLeuGlyGluAlaTyrPhe 140  
Db 972 GCCCTAGCCTCTGCGAGGGCGTTCGGCGGCGCTTCTACTGCTGGGGGAGGGGTATTTTC 1031

Qy 141 IleGluProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160  
Db 1032 ATCCAGCCGCTGCCGCCGCCAGCAGCGCTCGCCACCCGCCCGGAGGAGGAGCCG 1091  
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180  
Db 1092 CCGGCAACCACTACAGTTCACCTCTCTCGGCGGAATCGGCGGCGGAGCTAGCGGCGC 1151  
Qy 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200  
Db 1152 TGGGGGTCTGTGACGACGAGCCCGGCGGCTCGGAGGAGGAGGAGGAGGAGGAGGAG 1211  
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnTyrSerProGlnAspProAlaLeuGln 220  
Db 1212 GAGGGGACTGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1271  
Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240  
Db 1272 GCGGTAGGACAGCCACAGGAACTGGAAGCATAGAAGAAAGAGGATTTGTGTCCAGTCA 1331  
Qy 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260  
Db 1332 CGCTATGTGGAAACCATGCTTGTGGCAGACCACTCGATGCGAGATTTCCAGCGAGTGG 1391  
Qy 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280  
Db 1392 CTAAGCAATTACCTCTCAGTTGTTTCGGTGGCAGCCAGATTTGTACAAACACCCCGC 1451  
Qy 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300  
Db 1452 ATTCTGTAATTCAGTTAGCTGTGGTGGTGAAGATCTTGTTCATCCAGCATGAACAGA 1511  
Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTyrGlnLys 320  
Db 1512 GGGCGGAGAGTGACCTCCATGCTGCTCCCTCACCTCGCGGACTTTTGCAACTGGCAGA 1571  
Qy 321 GlnHisAsnProSerSerArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
Db 1572 CAGCACAACCCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATTTCTTTTACC 1631  
Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
Db 1632 AGACAGGACTTGTGTGGTCCCAGACATGTGATCTTTGGGATGGCTGATTTGGAACT 1691  
Qy 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380  
Db 1692 GTGTGTGATCCGAGCAGAGAGTGTCTCCGTATAGAAGATGATGGTTTACAAAGTGGCTTC 1751  
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400  
Db 1752 ACCACAGCCCATGAATTAGCCACCGTGTATACATGCCACATGATGATGATGATGATGAT 1811  
Qy 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420  
Db 1812 GCCAGCTTAATGGTGTGAACCAAGGATTTCCCATGATGGCGTCAATGCTTTTCCAACCTG 1871  
Qy 421 AspHisSerGlnProTyrSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
Db 1872 GACCACAGCCAGCGCTGTGCTCTCTTCAGTGGCTACATGATACATCATTTCTGGATAAT 1931  
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
Db 1932 GGTTCATGGGAATGTTGATGGACAGCTCAGAAATCCCATACAGCTCCACAGGAGTCTC 1991  
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
Db 1992 CTTGGCACCTCGTACCATGCCAACCGGAGTGCAGTTTACATTTTGGGAGGAGCTCCAAA 2051  
Qy 481 HisCysProAsnAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGly 500  
Db 2052 CACTGCCCGCATGCAGCCAGCACATGACACCTTCTGTGTGTATCCGSCACCTCTGTGGG 2111

QY 501 ValLeuValCysGlnThrLysHisPheProTTPAlaAspGlyThrSerCysGlyGluGly 520  
DB 2112 GTGCTGGTGTGTAACCAACACACTTCCGTGGGCGGATGGCCAGCTGTGGAGAGG 2171  
QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
DB 2172 AAATGGTGATCAACCGCAAGTGTGTGAACAAACCCAGACAGAAAGCATTTTCATACGGCT 2231  
QY 541 PheHisGlySerTrpGlyMetTrpGlyProTTPGlyAspCysSerArgThrCysGlyGly 560  
DB 2232 TTTCATGAAGCTGGGGAATGTGGGGGCTTGTGGGAGACTGTTCAGAGACGTGGCGTGA 2291  
QY 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyr 580  
DB 2292 GGAGTCCAGTACACGATCAGGGAATGTGACCAACCCAGTCCCAAGAAATGGAGGAATAC 2351  
QY 581 CysGluGlyLysArgValArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
DB 2352 TGTGAAGGCAACAGAGTGGCTTACAGATCCCTGTAACTTGAGGACTGTCCAGACAATAAT 2411  
QY 601 GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
DB 2412 GGAATAACCTTAGAGAGGACAATGTGANGACACACACGAGTTTCAAAGCTTCCTTT 2471  
QY 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640  
DB 2472 CGGAGTGGGCTCGCGTGGAAATGGATTCACAGTACGCTGGCTCTCCAAAGACACAGG 2531  
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DB 2532 TGCAGCTCATCTGCCAGCCAAAGGCATTTGGCTACTTCTCGTTTTCAGCCCCAGGTT 2591  
QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyCysVal 680  
DB 2592 GTAGATGGTACTCCATGTAGCCCAATCCACCTCTGTCTGTGTCAGAGACAGTGTGTA 2651  
QY 681 LysAlaGlyCysAspArgIleLysSerLysLysLysPheAspLysCysGlyValCys 700  
DB 2652 AAAGCTGTGTGATCGCATATAGACTCCAAAGAAAGACTTTGATAATGTGGTGTTC 2711  
QY 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720  
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DB 2772 TATCATGATATCATCACAAATTCACACTGGGCCCAACCAATCGAAGTGAACACGCGAAC 2831  
QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760  
DB 2832 CAGAGGGATCCAGGAACAATGGCAGCTTTCTGCCATCAAGCTGCTGATGGCACATAT 2891  
QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780  
DB 2892 ATTTCTTAATGGTGACTACACTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGGTGT 2951  
QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800  
DB 2952 GTCTTGAGTACAGCGGCTCTCTCGCGCATGTGAAAGAAATTCGACGCTTTAGCCCTCTC 3011  
QY 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820  
DB 3012 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCATGCGCTTCGACCTTAAATAATAA 3071  
QY 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840  
DB 3072 TACACCTACTTCTGTAAAGAAAGAAAGAAATCTTTCAATGCTATCCCCACCTTTTTCAGCA 3131  
QY 841 TrpValIleGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860  
DB 3132 TGGGTCAATGAAGAGTGGGCGAATTTCTTAAGTCATGTGAATGGGTGGCGAGAGA 3191  
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DB 3192 CTGGTAGAATGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTGCAAAAGGAAGTGAAG 3251  
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DB 3252 CCAGCCAGCACCAAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGGAGTGG 3311  
QY 901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920  
DB 3312 TCATCATGTTCTTAAGACCTGTGGGAGGGTTACAAAAAAGAGACTTGAAGTGTCTGTCC 3371  
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940  
DB 3372 CATGATCGAGCGGTGTATTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTAAACATTC 3431  
QY 941 IleAspPheCysThrMetAlaGluCysSer 950  
DB 3432 ATAGACTTTTGCACATGGCAGAAATGCAGT 3461  
RESULT 9  
US-09-989-687-125  
; Sequence 125, Application US/09989687  
; Publication No. US20040002449A1  
; GENERAL INFORMATION:  
; APPLICANT: Hastings, Gregg A.  
; INVENTOR: Ruben, Steven M.  
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
; FILE REFERENCE: 1488.107000D  
; CURRENT APPLICATION NUMBER: US/09/989,687  
; CURRENT FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 125  
; LENGTH: 4014  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (466)..(3366)  
; OTHER INFORMATION:  
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Alignment Scores:  
Pred. No.: 0 Length: 4014  
Score: 5144.00 Matches: 940  
Percent Similarity: 99.37% Conservative: 4  
Best Local Similarity: 98.95% Mismatches: 6  
Query Match: 99.13% Indels: 0  
DB: 11 Gaps: 0  
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DB 517 ATGGGAACCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCCGTACCACGCTGCTG 576  
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40  
DB 577 CTGCTCGCCGCGCGCTACTGGCGGTGCGAGCGACTCGGGCGCCCTCCGAGGAGAC 636  
QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60  
DB 637 GAGGAGCTAGTGTGCGGAGCTGGAGCGCGTCCCGGACACCGGACACGCGCTCCCG 696  
QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80  
DB 697 CTGCAGCCTTTGACGACGAGCTGGATCTGGAGCTGCGCGCCGACGAGCAGCTTTTGGCG 756  
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGlyThrProLeuProGlu 100  
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QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120

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Db 817 ACCGACCTCGCGACCTGCTTCTACTCCGCGACCGTGAATGGCGATCCCAAGCTCGGCTGC 876  
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Db 877 GGCCTCAGCCTTCGCGAGCGCGTGC CGCGCGCTTCTACTCGTGGGGAGCGTATTTC 936  
Qy 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160  
Db 937 ATCCAGCGCTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCCAGGGAGAGCGG 996  
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlnGlyAspValGlyGlyThr 180  
Db 997 CGCGCACCACTACAGATTCCACCTCTCGCGCGGAATCGCGAGCGCGAGCTAGCGCGCACG 1056  
Qy 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGlnThrGluAspGluAsp 200  
Db 1057 TGGCGGGTGTGTGACGACGAGCGCCCGCGCGACTGGGAGAGCGAGACCGAAGCGAGAC 1116  
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnThrProGlnAspProAlaLeuGln 220  
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Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHis 240  
Db 1177 GCGTAGGACAGCCACAGGAATGGAAGCATAGAAAGAGCGAATTTGTGCCAGTCC 1236  
Qy 241 ArgTyrValGlnThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260  
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Qy 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280  
Db 1297 CTAAAGCATTAACCTTCTCAGTTGTTTCGGTGGCGAGCAGATTGTACAAACCCCGACG 1356  
Qy 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGlnGlnLys 300  
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Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320  
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Qy 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340  
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Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360  
Db 1537 AGACAGACTTGTGTGGTCCCGACATGTGATCTCTTGGGATGGCTGATGTGGAAT 1596  
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Db 1597 GTGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAAAGATGATGGTTTACAAGTGGCTTC 1656  
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400  
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Qy 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440  
Db 1777 GACCACAGCCGCGCTTGGTCTCTTCAGTGGCTACATGAATACATCATTTCTGGATAT 1836  
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460  
Db 1837 GGTCAATGGGGAATGTTTGTATGGCAAGCCTCAGAAATCCCATACAGCTCCCGCGCATCTC 1896  
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
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1897 CCTGCACCTCGTACGATGCCAACCGGCAGTGCCTAGTTTACATTGGGGAGGACTCCAAA 1956  
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Db 1957 CACTCCCTCTGTCAGCCAGCACATGTAGACCTTGTGTGTACCGGCACCTCTGGTGGG 2016  
Qy 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520  
Db 2017 GTGCTGGTGTGTCAAAACCAACACTTCCCTGGGGCGGATGGCACCAGCTGTGGAGAGGG 2076  
Qy 521 LysTyrCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540  
Db 2077 AAATGGTGTATCAACCGCAGTGTGTGAACAAACACACAGAAAGCATTTTGTATAGCTCT 2136  
Qy 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560  
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Qy 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580  
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Qy 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600  
Db 2257 TGTGAAGCAACAGTGGCTACAGATCTCTGTAACTTGAGGACTGTCCAGACATAAT 2316  
Qy 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620  
Db 2317 GGAAAAACCTTTAGAGAGGAAACAATGTGAAGCACACAAACGAGTTTCAAAAGCTTCCTTT 2376  
Qy 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640  
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Qy 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680  
Db 2497 FTAGATGGTACTTCCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGA 2556  
Qy 681 LysAlaGlyCysAspArgIleAspSerLysLysPheAspLysCysGlyValCys 700  
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Qy 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720  
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Qy 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740  
Db 2677 TATCATGATATCATCACTTCCAACTGGAGSCCAACATCGAAGTGAACAGCGGAAC 2736  
Qy 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760  
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Qy 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780  
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Db 2917 AAAGAGCCCTTGACCATCAGGTTCTTACTGTGGCAATGCCCTTCGACCTTAATAATTAA 2976  
Qy 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840  
Db 2977 TACACCTACTTCGTAAGAGAGAGAGGAATCTTTCAATGCTATGCCACATTTTTCAGCA 3036

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QY 841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db 3037 TGGGTCATTGAAGAGTGGGGCGCAATGTTCTAAGTTCATGTGAATTTGGTTGGCAGAGAAGA 3096
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaIysGluVallys 880
Db 3097 CTGGTAGAATGCCGAGACATTAATGGACAGCTGCTTCGAGTGTGCAAAAGGAAGTGAAG 3156
QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db 3157 CCAGCCAGACCCAGACCTTGTGCAGACCATCTCTGCCCCAGTGGCAGCTGGGGAGTGG 3216
QY 901 SerSerCysSerLysThrCysGlyLysGlyTrpLysLysArgSerLeuLysCysLeuSer 920
Db 3217 TCATCATGTGTTAAGACCTGTGGGAAGGGTTACAAAAAACAAGCTTGAAGTGTCTGTCC 3276
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db 3277 CATGATGAGGAGGGTGTATCTCATGACAGCTGTGATCTTTAAGAAACCTTAACATTTTC 3336
QY 941 IleAspPheCysThrMetAlaGluCysSer 950
Db 3337 ATAGACTTTTGCACAATGCGAGATGCAGT 3366

RESULT 10
US-10-425-114-26851
; Sequence 26851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26851
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-036-D4_FLI
US-10-425-114-26851

Alignment Scores:
Pred. No.: 0 Length: 4848
Score: 5097.50 Matches: 949
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 98.24% Indels: 73
Db: 13 Gaps: 1

US-09-373-658C-2 (1-950) x US-10-425-114-26851 (1-4848)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 493 ATGGGAGACGGGAGCGGCTCCGGGGTCTCGAGCTTTGGCCCGTACCCACGCTGCTG 552
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db 553 CTGCTCGCGCGGCGCTACTGGCCGTGTCGAGCGACCTCGGGCGCCCTCTCGAGAGGAC 612
QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db 613 GAGGAGCTAGTGGTCCCGAGCTGAGCGCGCCCGGACACCGGACCGCGCTCCG 672
QY 61 LeuHisAlaPheAspGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
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Db 673 CTGCACGCTTTGACACGACAGCTGGATCTGGAGCTGGCGCCGACAGCAGCTTTTGGCG 732
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db 733 CCCGCTTCACGCTCCAGACGTCGGGCGCAATCCCGGTCGAGACGCCCTTCGCGAA 792
QY 101 ThrAspLeuAlaHisCysPheTyzSerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db 793 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGCTGAATGGCGATCCAGCTCGGCTGCC 852
QY 121 AlaLeuSerLeuCysGluGlyValArgGlyValAlaPheTyzLeuLeuGlyGluAlaTyPhe 140
Db 853 GCCCTCAGCCTTCTCGAGGGGCTGCGCGCGCTTCTACCTGCTGGGGAGCGGTATTC 912
QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlyLysPro 160
Db 913 ATCCAGCGCTGCGCGCGCGCGCGCTGCGCACCGCGCCCGCGAGGAGAGCGG 972
QY 161 ProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyThr 180
Db 973 CCGGCACCATCTACAGTTTCCACCTCTCTCGCGCGAATCGGAGGCGGACGCTAGGCGGACG 1032
QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 1033 TCGGGGTGGTGAGACGAGCGCGCGCGCTGGGAAAGCGGAGACCGAAGACGAGGAC 1092
QY 201 GluGlyThrGlnGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db 1093 GAAGGACTCGAGGCGGAGGAGCGAAGGCGCTCAGTGGTGGCGGAGGACCGCGCACTGCA 1152
QY 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHis 240
Db 1153 GCGTAGGACAGCCACAGGAACCTGGAAAGCATAGAAGAGCGATTTGTCTCAGTCA 1212
QY 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db 1213 CGCTATGTGAAACCATGCTTGTGGAGACGAGTCGATGCGAGAAATTCGACGCGAGTGT 1272
QY 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
Db 1273 CTAAGCATTTACCTTCTCAGCTGTTTTCGGTGGCAGCCAGATTGTACAACACCCCGC 1332
QY 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300
Db 1333 ATTCGTAATTCAGTTAGCTGGTGGTGAAGATCTTGTCTATCCAGATGAACAGAG 1392
QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 1393 GGGCGGAGTGACCTCCAAATGCTGCCCTCACTCTCGGAACTTTGCAACTGGCAGAAG 1452
QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
Db 1453 CAGCACAACCCACCCAGTGCAGGGATGCAGAGCACTATGACACAGCAATTCITTTCCACC 1512
QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1513 AGACAGCACTTGTGTGGTCCGACATGATGATCTCTGGGATGGCTGTGTGGAACT 1572
QY 361 ValCysAspProSerArgSerCysSerValIleLeuAspAspGlyLeuGlnAlaAlaPhe 380
Db 1573 GTGTGTATCCGAGCAGACAGCTGCTCGCTATAGAGATGATGGTTTACAGCTGCCTTC 1632
QY 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCys 400
Db 1633 ACCACAGCCCATGAATTAGGCCACGCTGTTTAAATGATGATGATGATGATGATGATGAT 1692
QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1693 GCACGCTTATATGATGTAACACGAGGATCCCATGATGATGATGATGATGATGATGATG 1752
QY 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
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Db 1753 GACCACAGCCAGCCTTGCTCTCCTGAGTCCTACATGATTACATCAATCTTCGGATAAT 1812  
Qy 441 GlyHisGlyGluCysLeuMetAspGlyProGlnAsnProIleGlnLeuProGlyAspLeu 460  
Db 1813 GGTCAATGGGAATGTTTGGATGGCAAGCCTCAGAATCCATA-CAGCTCCCGAGCGATCTC 1871  
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480  
Db 1872 CTTGGCACTCTGTCAGATGCCACCGGAGTCCCGATTTTCATTTGGGGAGGACTCCAAA 1931  
Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGly 500  
Db 1932 CACTGCCCTCATGCGAGCAGCACATGTAGCACCTTGTGGTGATACCGGCACCTCTGGTGGG 1991  
Qy 501 ValLeuValCysGlnThrLysHisPheProTyrAlaAspGlyThrSerCysGlyGluGly 520  
Db 1992 GTGCTGTGTGTCAAAACCAACACTTCCCGGGGGGAGTGGCAGCCTGTGGAGAGGG 2051  
Qy 521 LysTyrCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAsp----- 538  
Db 2052 AAATGGTGTATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGATGTGAGT 2111  
Qy 538 ----- 538  
Db 2112 TTTTCTACTGAACACATTCAGAAATTGAAAGAAACAAAGTGTATGTAAGATATGATAC 2171  
Qy 538 ----- 538  
Db 2172 CAAGTTAAACATCCCAATCCGTCTCTAGCAGGAATGCGAGATAGCTTAATTTTAGAA 2231  
Qy 538 ----- 538  
Db 2232 CTGATCTTTGTCCCATGTGGCTTCTTTGATACCTTAAAGTTCTCTTTAGATAAATCT 2291  
Qy 539 ----- ThrProPheHisGlySerTyrGlyMetTyrGly 549  
Db 2292 AATGCTGATGATTTATGCTCTCCATTAGACGCTTTTTCATGGAAAGCTGGGGAAATGGGG 2351  
Qy 549 yProTyrGlyAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCys 569  
Db 2352 GCCTTGGGGAGACTTTCGAGAACGTCGCGTGGAGGAGTCCAGTACACGATGAGGAAATG 2411  
Qy 569 sAspAsnProValProLysAsnGlyLysTyrCysGluGlyValArgValArgTyrAr 589  
Db 2412 TGACAAACCCAGTCCCAAGAAATGAGGAAAGTACTGTGAAGGCAAAACGATGCGCTACAG 2471  
Qy 589 gSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCys 609  
Db 2472 ATCTGTAACTTTGAGGACTGTCCAGACATATATGGAAACCTTTAGAGAGAAACATG 2531  
Qy 609 sGluAlaHisAsnGlnPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrIle 629  
Db 2532 TGAAGCACACACAGAGTTTTTCAAAAGCTTCCITTTGGGAGTGGGCTGCGGTGGAATGGAT 2591  
Qy 629 eProLysTyrAlaGlyValSerProLysAspArgCysValLeuLeuLeuLeuLeuLeu 649  
Db 2592 TCCCAAGTACCTGGCTGTCCACAAAGGACAGTGCAGCTCATCTGCCAACCCAAAGG 2651  
Qy 649 yIleGlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAs 669  
Db 2652 CATTTGGTACTTCTCTGTTTGGAGCCCAAGTTGTAGATGGTACTCCATGTAGCCACGA 2711  
Qy 669 pSerThrSerValCysValGlnGlnCysValLysValLysAlaGlyCysAspArgIleLeu 689  
Db 2712 TTCACCTCTCTGTGTGCAAGACAGTGTGTAAGCTGGTGTGTGATCGCATCATAGA 2771  
Qy 689 pSerLysLysPheAspLysCysGlyValCysGlyValAsnGlySerThrCysLysLys 709  
Db 2772 CTCCAAAAAGAGTTGATAAATGTGGTGTTCGGGGGAAATGGATCTACTTGTAAAAA 2831  
Qy 709 sIleSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProTh 729  
Db 2832 AATATCAGGATCAGTTACTAGTGCAAACCTGGATATCATGATATCATCAATTCACAC 2891

Qy 729 rGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySe 749  
Db 2892 TGAGAGCACCAACATCGAAGTGAACACAGCGGAACCCAGAGGGGATCCAGGAACAAATGGCAG 2951  
Qy 749 rPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSe 769  
Db 2952 CTTTCTTGCCATCAAGCTGCTGATGGCACATATATCTTAAATGGTGACTACTTGTTC 3011  
Qy 769 rThrLeuGluGlnAspIleMetTyrLysGlyValValLeuLeuArgTyrSerGlySerSerAl 789  
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Qy 789 aAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLe 809  
Db 3072 GCGTTTGGAAAGATTCGAGCTTTAGCCCTCTCAAGAGGCCCTTCACCATCCAGGTTCT 3131  
Qy 809 uThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLys 829  
Db 3132 TACTGTGGGCAATGCCCTTCGACCTTAAATTAATACACCTACTTCTGTAAGAGAGAGAA 3191  
Qy 829 sGluSerPheAsnAlaIleProThrPheSerAlaTyrValIleGluGluTyrGlyGluCys 849  
Db 3192 GGAATCTTTCAATGCTATCCCACTTTTTCAGATGGGTCAATTGAAGATGGGGCGAATG 3251  
Qy 849 sSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGly 869  
Db 3252 TTCTAAGTCATGTGAATTCGGTGGCAGAGAGACTGGTAGAATGCCAGACATTAATGG 3311  
Qy 869 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 889  
Db 3312 ACAGCCTGTCTTCGAGTGTGCAAGAGAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAG 3371  
Qy 889 pHisProCysProGlnTyrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLys 909  
Db 3372 CCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCACTATGTTCTAAGACCTGTGGAA 3431  
Qy 909 sGlyTyrLysLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHis 929  
Db 3432 GGGTTACAAAAAAGAAAGCTTGAAGTGTCTGCCATGATGAGGGGTGTATCTCATGA 3491  
Qy 929 uSerCysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCys 949  
Db 3492 GAGCTGTGATCTCTTTAAAGAAACCTTAAACATTTTCATAGACTTTTCCACAAATGGCAGATG 3551  
Qy 949 sSer 950  
Db 3552 CAGT 3555  
RESULT 11  
US-09-373-658-20  
; Sequence 20, Application US/09373658  
; Publication NO. US20030092900A1  
; GENERAL INFORMATION:  
; APPLICANT: Ituela-Arispe, Luisa  
; APPLICANT: Hastings, Gregg A.  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Jonak, Zdenka I.  
; APPLICANT: Trulli, Stephen H.  
; APPLICANT: Fronwald, James A.  
; APPLICANT: Terrett, Jonathan A.  
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
; FILE REFERENCE: 1489.1070006  
; CURRENT APPLICATION NUMBER: US/09/373,658  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 4180  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism:Unknown

US-09-373-658-20

Alignment Scores:

Pred. No.: 0  
Score: 4299.50  
Percent Similarity: 88.31%  
Best Local Similarity: 82.36%  
Query Match: 82.86%  
DB: 10  
Gaps: 5

US-09-373-658C-2 (1-950) x US-09-373-658-20 (1-4180)

QY	1	MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu	20
DB	441	ATGGGGAGCTCCAGCGGGCAGCGAGATCTCGGGGCTCTCTGCGCAGACACATGCTGTG	500
QY	21	LeuLeuAlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer	37
DB	501	CTGCTCTCTGCTTCCATAACAAGCTGCTATGTGCGCGGGCGCACACACGGCGGCCACG	560
QY	38	GluGluAspGluGluLeuValProGluLeuGluArgAlaProGlyHisGly-----	55
DB	561	GAGGAGATGAGAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	620
QY	56	ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAsp	75
DB	621	ACCACAGCGCTTCTGTCAGCGCTTTGGCCAGCAGCTACATCTGAAGTTGCGCGGAC	680
QY	76	SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerGlu	95
DB	681	AGCGGTTCCTGCGCGCTGCTTACCTCTGAGACTGTGCGGGCGCAGTCCCGGTCCGAG	740
QY	96	ThrProLeu-----ProGluThrAspLeuAlaHisCysPheTy-SerGlyThrValAsn	113
DB	741	GCACAACATCTGGACCCACCGGGACCTGGCTCATCTGCTCTGCGCAGGTAAC	800
QY	114	GlyAspProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTy	133
DB	801	GGTGAATCCCGCTGTCGCCAGCCCTCAGCTCTGTGAAGGTGTGCTGCTGCTCTAC	860
QY	134	LeuLeuGlyGluAlaTyPheLeuGlnProLeuPro---AlaAlaSerGluArgLeuAla	152
DB	861	CTACAGGAGAGAGGTTCCTTCATTGACGCGCTGGAGTGCGCACCGCGCTGGCC	920
QY	153	ThrAlaAlaProGlyGluTyProAlaProLeuGlnPheHisLeuLeuArgArgAsn	172
DB	921	CCTGCGCTCCCGAGGAGAGTCACTCCGACGCGCGCAGTTCACATCTCGAGGCGAAG	980
QY	173	ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly	192
DB	981	CGCGGGGAGTGGCGGCCCAAGTGCGCGCTCATGAGCAGCAGACCCCTGCCAAC	1037
QY	193	LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp	212
DB	1038	-----AGCGACTCGCGACCCGAGAGCGCAGAACACCCCGGAACCACTGG	1079
QY	213	SerProGlnAspProAlaLeuGlnGlyValGlnProThrGlyThrGlySerIleArg	232
DB	1080	CCTGTGCGGAGACCCACCGCTCAGGACCGCGGAAAGCCATCAGGACCGAGGAGCATAAG	1139
QY	233	LysLysArgPheValSerSerHisArgTyValGluThrMetLeuValAlaAspGlnSer	252
DB	1140	AAGAAGCATTTGTCTCAGCCCGCTTATGTGGAACCACTCTGCTAGCTGACAGTCC	1199
QY	253	MetAlaGluPheHisGlySerGlyLeuLysHisTyLeuLeuThrLeuPheSerValAla	272
DB	1200	ATGGCGGACTTCCAGCGGCGGTCTAAAGCATTAACCTTCTAAACCTGCTCTCGGTGCA	1259
QY	273	AlaArgLeuTyTyHisHisProSerIleArgAsnSerValSerLeuValValValIle	292
DB	1260	GCCAGGTTTACAGCATCCAGCATTAAGGATTCATTAAGCTTGGTGGTGGTGGATC	1319
QY	293	LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu	312

DB	1320	TTGGTCATATACGAGCAGCAGAGGAGCCAGAGTTACCTCCATGACGCTCTCACCTT	1379
QY	313	ArgAsnPheCysAsnTrpClnLysGlnHisAsnProProSerAspArgAspAlaGluHis	332
DB	1380	CGGAATTTCTGAGCTGGCAGAAACAACAACACCCAGTGCAGGGATCCAGAGCAC	1439
QY	333	TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr	352
DB	1440	TATGACACTGCAATCTGTTTCCACAGACAGGATTATGTGGCTCCACACGTTGACACT	1499
QY	353	LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu	372
DB	1500	CTCGGAATGGCAGATGTTGGAAACCGTATGTGACCCAGCAGAGCTGCTCAGTCATAGAA	1559
QY	373	AspAspGlyLeuGlnAlaAlaPheThrAlaHisGluLeuGlyHisValPheAsnMet	392
DB	1560	GATGATGTTTGCAGCCGCTTACACAGCCCATGATTTGGGCAATGTTTACATG	1619
QY	393	ProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMet	412
DB	1620	COGCAAGATGATGCTTAAGCACTGTGCCAGCTTGAATGTTGAGTGGGATTTCTCATCTG	1679
QY	413	MetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTy	432
DB	1680	ATGGCTCTGATGCTCTCCAGCTTAGCCATAGCCAGCCCTGCTCAGCTTGCAGTGCCTAC	1739
QY	433	MetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsn	452
DB	1740	ATGGTCAGCTCTTCTAGATAATGGAACAAGGAAATGTTTATGACACAGCCCGAGAT	1799
QY	453	ProIleGlnLeuProGlyAspLeuProGlyThrSerTyAspAlaAsnArgGlnCysGln	472
DB	1800	CCATCAAGCTCCCTTCTGATCTTCCCGGTACCTTGTACGATGCCAACCTTCCCTTGGCA	1859
QY	473	PheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeu	492
DB	1860	TTTACATTCGAGAGGAAATCAAGCACTGCCCTGATGAGCCAGCACATGATACCTG	1919
QY	493	TrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAla	512
DB	1920	TGGTGCACTGCGACCTCCGTTGCTTACTGTTGTCGCAAGTGCAGTGCCTGCAAGACA	1979
QY	513	AspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThr	532
DB	1980	GATGCAACAGCTGTGGAGAGGAGGAGTGTGTGTGCTGAGTGCAGTGCCTGCAAGACA	2039
QY	533	AspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGly	552
DB	2040	GACATGAAGCATTTTGTCTCTCTGTTTCATGGAAGCTGGGACCCATGGGACCGTGGGA	2099
QY	553	AspCysSerArgThrCysGlyGlyValClnTyThrMetArgGluCysAspAsnPro	572
DB	2100	GACTGCTCAAGAACCTGT	2159
QY	573	ValProLysAsnGlyLysTyCysGluGlyLysArgValArgTyArgSerCysAsn	592
DB	2160	GTCCCAAGAACCGAGGAGAGTACTGTGAAGGCAACAGCTCCGCTACAGTCTCTGTAAC	2219
QY	593	LeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHis	612
DB	2220	ATCAGGACTGTCCAGCAATAACCGAAAAACGTTTGTAGAGGAGGAGTGTGAGGCGCAC	2279
QY	613	AsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTy	632
DB	2280	AATGAGTTTCCAAAGCTCTCTTTGGGAATGAGCCCACTGTAGAGTGGACACCAAGTAC	2339
QY	633	AlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTy	652
DB	2340	GCCGGCTCTCGCAAGAGGACAGTGCACCTGTGAAAGCCCAAGGATTTGGCTAC	2399
QY	653	PhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSer	672

Db 2400 TTTTTCGTCTTACAGCCCAAGGTGTAGATGGGACCTCCCTGTAGTCACAGACTCTACCTCT 2459  
Qy 673 ValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLys 692  
Db 2460 GTCTGTGTCAAGGGCAGTGTGTGAAGCTGGCTGTGATCGCATCATAGACTCCAAAAG 2519  
Qy 693 LysPheAspLysCysGlyValCysGlyGlyValGlySerThrCysLysLysLysSerGly 712  
Db 2520 AAGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2579  
Qy 713 SerValThrSerAlaLysProGlyThrHisAspIleIleIleIleIleIleIleIleIle 732  
Db 2580 ATAGTCACCTAGTACAAAGCTGGGTATCATGATCATGATCATGATCATGATCATGAT 2639  
Qy 733 AsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAla 752  
Db 2640 AACATTGAGTGAACATCGAATCAAGAGGGGTCCAGAAACAAATGGCAGCTTTCGGCT 2699  
Qy 753 IleLysAlaAlaAspGlyThrThrIleLeuAsnGlyAspThrThrLeuSerThrLeuGlu 772  
Db 2700 ATTAGAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2759  
Qy 773 GlnAspIleValThrLysGlyValValLeuArgThrSerGlySerSerAlaAlaLeuGlu 792  
Db 2760 CAAGACCTCACCTACAAAGGTACTGTCTTAAGGTACAGTGGTTCTCGGCTCGCTGGAA 2819  
Qy 793 ArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGly 812  
Db 2820 AGAATCGGAGCTTTAGTCCACTCAAGAACCTTTAAACATCCAGTCTTATGTTAGGC 2879  
Qy 813 AsnAlaLeuArgProLysIleLysThrThrPheValLysLysLysLysLysLysLysPhe 832  
Db 2880 CATGCTCTCGAGCCCAAAATTAATTCACCTACTTATGAAAGAGAGAGAGAGAGAGATTC 2939  
Qy 833 AsnAlaIleProThrPheSerAlaTropValIleGluGluThrGlyGluCysSerLysSer 852  
Db 2940 AAGCCATTTCCCAATTTTCTGAGTGGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2999  
Qy 853 CysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAla 872  
Db 3000 TCGGGCTCAGTTGGCAGAGAGAGTAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGT 3059  
Qy 873 SerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892  
Db 3060 TCCGAATGTCCAAAGGAAGTGAAGCCAGCCAGCAGTACCAGACCTTGTGCAGACCTTCTTC 3119  
Qy 893 ProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTrpLys 912  
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Qy 913 LysArgSerLeuLysCysLeuSerHisAspGlyValLeuSerHisGluSerCysAsp 932  
Db 3180 AAGAGAACCTTGAATGTGTGCCAGATGCCAGATGGGGGGGTGTATCAATGAGAGCTGTGAT 3239  
Qy 933 ProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950  
Db 3240 CCITTGAAGAGCCAAAGCAATTAATGATTTTGCACATGACACAGTGCAGT 3293

## RESULT 12

US-09-389-687-20  
; Sequence 20, Application US/09989687  
; Publication No. US2004002449A1  
; GENERAL INFORMATION:  
; APPLICANT: Hastings, Gregg A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
; FILE REFERENCE: 1488.107000D  
; CURRENT APPLICATION NUMBER: US/09/989,687  
; CURRENT FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 4180

TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Unknown  
US-09-989-687-20

Alignment Scores:  
Pred. No.: 0 Length: 4180  
Score: 4299.50 Matches: 789  
Percent Similarity: 89.31% Conservatives: 57  
Best Local Similarity: 82.36% Mismatches: 97  
Query Match: 82.86% Indels: 15  
DB: 11 Gaps: 5

US-09-373-658C-2 (1-950) x US-09-989-687-20 (1-4180)  
Qy 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
Db 441 ATGGGGGACGTCACCGGGCAGCGAGATCTCGGGGCTCTCTGTCGCGCACACATGCTGTG 500  
Qy 21 LeuLeuAlaAlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37  
Db 501 CTGCTCTCTGCTTCCATACAAATGCTGTATGTGCGGGGGCGCACCGGGGCCCCACG 560  
Qy 38 GluGluAspGluGluLeuValProGluLeuGluArgAlaProGlyHisGly----- 55  
Db 561 GAGGAAGATGAGAGCTGCTGCTCGCTCGAGCGCGCCCGCGCGCCACGATTCACCC 620  
Qy 56 ThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAsp 75  
Db 621 ACCACACGCTTCTGCTGAGCGCTTGGCAGCAGCTACATCTGAAGTTGGACGCGGAC 680  
Qy 76 SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGlu 95  
Db 681 AGCGGTTCTTGGCGCTGGCTTACCTCGACAGCTGTGGGGCGCAGTCCCGGCTCCGAG 740  
Qy 96 ThrProLeu-----ProGluThrAspLeuAlaHisCysPheThrSerGlyThrValAsn 113  
Db 741 GCACAACATCTGGACCCCGACCGGGGACCTGGCTCACTGCTCTCTGCGACGTTGAC 800  
Qy 114 GlyAspProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyr 133  
Db 801 GGTGATCCCGGCTCTGCGCGACGCTCAGCCTCTGGAAGGTGTGCTGCTGCTCTCTAC 860  
Qy 134 LeuLeuGlyGluAlaTyrPheIleGlnProLeuPro-----AlaAlaSerGluArgLeuAla 152  
Db 861 CTACAAGGAGAGAGAGTCTTCTTATTCAGCCGCTGGAGTGGCCCGACCGAGCCCTGGCC 920  
Qy 153 ThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172  
Db 921 CTGCGCTGCGCGACGAGAGAGTATCCGACCGCCCGAGTTCACATCTCTGAGGCGAAG 980  
Qy 173 ArgGlnGlyAspValGlyThrCysGlyValValAspAspGluProArgProThrGly 192  
Db 981 CGCGGGGCGAGTGGCGGCGCCCAAGTGGCGGCTCATGACGCGCCCGACCGAGCCCTGCAACC 1037  
Qy 193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212  
Db 1038 -----AGCGACTCGCGACCCGAGAGCCAGAACACCCCGAACCAGTGG 1079  
Qy 213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232  
Db 1080 CTGTGCGGGACCCCGACCGCTCAGGACCGCGGGAAGCCATCAGGACCGAGAAAGATAAGG 1139  
Qy 233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252  
Db 1140 AAGAAGCGAATTTGTGTCCAGCCCCCGTTATGTGGAACCATGCTCTAGTACGACGATCC 3199  
Qy 253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272  
Db 1200 ATGGCGGACTTCCACGCGAGCGGTCTAAGACATTACCTTCTAACCTGTTCTCGGTGGCA 1259  
Qy 273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIle 292



135	LeuGlyValAlaThrPheIleGlnProLeuProAla--AlaSerGluArgLeuAlaThr	153
866	CAAGGGCAGAGATTCTTCATTACGCCACAGCCCTTCGGTGGCCACCGAGCGCTGGTCCCC	925
154	AlaAlaProGlyValLysProProAlaProLeuGlnPheHisLeuLeuArgAsnArg	173
926	GC CGAACCGAAGGAGGATCAATCGCACCTCCCGCGTTCACATCTGTAGCGCGAAGCGG	985
174	GlnGlyAspValGlyThrCysGlyValValAspAspGluProArgProThrGlyLys	193
986	CGGGGACGCGCGGCCAACAGTCCGCTGTATCGACGAGAGACCTTGCACACC-----	1039
194	AlaGluThrGluAspGluAspGluGlyThrGluGlyValAspGluGlyProGlnTrpSer	213
1040	-----AGCAACTCCGGTCGCGAAGACCGACAGAACCCCGGACCACTGGCGCT	1084
214	ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys	233
1085	CTCGGAACCCCACTCTCTCAGGGCGGGGAAAGCCACACGACGACGAGAGCATNAAGAAAG	1144
234	LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet	253
1145	AAGCGATTTGTCTCCAGCCCCCGTTATGTGGAAACCATGCTCTGTGGCTGACCATCTCATG	1204
254	AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla	273
1205	GCTGACTCTCCACGCGAGCGGTCTAAAGCATTAACCTCTTAACCTCTCTCGTGGCGACCC	1264
274	ArgLeuTyrIleHisProSerIleArgAsnSerValSerLeuValValValLysIleIeu	293
1265	AGATTTTACAAGCACCCACGACATTAGGAATTCATTAAGTCTGGTGGTGGGAAGATCTTG	1324
294	ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg	313
1325	GTCTATATGAGGACGACGAGGACCGGAAGTTACTTCCATCGCGCTCTCACCCCTTAGG	1384
314	AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr	333
1385	AATTTCTGTAGCTGGCAGAAACAGCACAAACAGCCCCAGTCAACCGGGATCCAGACCATAT	1444
334	AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu	353
1445	GACACAGCGAATCTGTTCCACGACGAGGATTTATGTGGCTCCACACTGTGACACTCTC	1504
354	GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp	373
1505	GCGATGGCTGATGTTGGAACTGATGTATGACCCCGACGAGGAGCTGTTCCGTATCGAAGAT	1564
374	AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro	393
1565	GATGGTTTACAGCTGCCTTCAACACAGCCCATGAATTGGGCCATGTGTTTAACATGCCA	1624
394	HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet	413
1625	CACATGACGCCAAGCACTCGCGCCAGCTTTAATGCGGTGATGGGGATTCCTCATCTGATG	1684
414	AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet	433
1685	GCCTCGATGCTCTCCAGCTTGGACCAACAGCCCGCTGGTCTCTCTTCGATGGCTACATG	1744
434	IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro	453
1745	GTCACATCATCTCTGACACACCGGCCATGGGGATGTTTGATGNCANAGCCGACGACCCA	1804
454	IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe	473
1805	ATCAAGCTCCCATCTGATCTTCCCGGTACCTTGTAGATGCCAACCCGCCAGTGTCACTTT	1864
474	ThrPheGlyGlnAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp	493
1865	ACCTTCGGGAGAAATCCAGCGACTGCCCTGATGTCAGCCAGACATGCAGTACCCTGTGG	1924
494	CysThrGlyThrSerGlnGlyValLeuValCysGlnThrLysHisPheProTrpAlaAsp	513

1925 TGCACTGGCACCCTCGGTGGCTTACTGGTGTGCCAAACAAACACTTCCCTTGGGCAGAT 1984  
514 GlyThrSerCysGlyGluGlyValThrCysIleAsnGlyLysCysValAsnLysThrAsp 533  
1985 GGCACCAAGCTGGGAGAGGAAATGGTGTGTGCGGCGCAAGTGTGTGACACAGACCGAC 2044  
534 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 553  
2045 ATGAAGACATTTGCTACTCTCTGTCTCATGGAGCTGGGACCGTGGGGACCATGGGGAGAC 2104  
554 CysSerArgThrCysGlyGlyValGlnTyrThrMetArgGlyCysAspAsnProVal 573  
2105 TGCTCAAGAACCTGTGTGGAGAGTTCATATATACATGAGAGATGTGACAAACCCGGTTC 2164  
574 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593  
2165 CCAAGAGACCGGGGGAAGTACTCGGAAGGCAACAGTCCGCTACAGGTCTCTGTAAACATT 2224  
594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisLeu 613  
2225 GAGGACTGTCCAGACAAATAACGGAAACAAATTCAGAGAGGACCAATGCGAGCGGCACAA 2284  
614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrIleProLysTyrAla 633  
2285 GAGTTTTCACAGCTTCTCTTTCGGAATGAACCCAGCGTGAATGGACACCCCAAGTATGCT 2344  
634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653  
2345 GCGGTCTGCCAAAGGACAGGTGCAAGCTTACTCTCGAAGCCAAAGGCAATGGCTACTTTC 2404  
654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673  
2405 TTTGTTTACAGCCCAAGGTGTAGTATGCGACTCTCTGTAGTCCAGACTCTACTTCTGTC 2464  
674 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 693  
2465 TGTGTGCAAGGACAGTGTGTGAAGCTGCTGTGATCGCATCATAGACTCCAAAGAGAG 2524  
694 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 713  
2525 TTCGATAGTGTGGGTGTGTGAGGAATGCTCCAGTGCAGAAATATTCAGGAACG 2584  
714 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 733  
2585 GTCACTAGTACAAAGCTGGGTATCATGACATTTGTACAAATTCCTGCTGGAGCCCAAC 2644  
734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIle 753  
2645 ATTGAAGTGAAACATCGTAAATCCAAAGGGGATCCAGAAACATGGCAGCTTTCTGCTATT 2704  
754 LysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln 773  
2705 AGAGCTGCAGATGGTACCTATATTCTGAATGGAACCTTCACTCTGTCCACTCTAGAGCAA 2764  
774 AspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg 793  
2765 GACCTCACCTACAAAGGACTGTCTTAAGATACAGTGTCTCTCAGCAGCATTTGAAGA 2824  
794 IleArgSerPheSerProLysLysGluProLeuThrIleGlnValLeuThrValGlyAsn 813  
2825 ATCCGAGCTTTAGTCCACTCAAGAACCCCTGACCATCCAGGTCTTATGTGTGGCCAT 2884  
814 AlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGlySerPheAsn 833  
2885 GCTCTCCGACCCAAATCAAGTACACCTATTATTATGAAGAGAAAGACGCGCCCTTCAAC 2944  
834 AlaIleProThrPheSerAlaTrpValIleGluGluTyrGlyGluCysSerLysSerCys 853  
2945 GCTATTCCRCATTTTCGAGTGGGTGATTTGAAGAGTGGGGGAGTGTCTCCAAAGCATGT 3004  
854 GluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSer 873

3005 GGTTCCTGGTGGCAGAGAGAGTGGTAGAGTGCAGAGACATTAATGACACCTGCTTCT 3064  
874 GluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPro 893  
3065 GAATGTGCCAAAGAGTGAAGCCAGGACGATACACAGACTTGTGCGAGACCTTCTTGGCCCA 3124  
894 GlnTrpGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLysLys 913  
3125 CGTTGGCAGGTGGGGGATTTGTCACCATGTTCTAAACTTGTGGGAAGGGTATTAAGAAG 3184  
914 ArgSerLeuLysCysLeuSerHisAspGlyValLeuSerHisGluSerCysAspPro 933  
3185 AGAACCTTGAATGTCGTGCCATGATGGCGGTGTGTTATCAATGAGAGCTGTGATCCT 3244  
934 LeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950  
3245 TTGAAGAAACCAAGCAATTAATGACTTTTGCATACTGACACAGTGCAGT 3295

## RESULT 14

US-10-191-803-170  
; Sequence 170, Application US/10191803  
; Publication No. US20040014040A1  
; GENERAL INFORMATION:  
; APPLICANT: MENDRICK, Donna  
; APPLICANT: PORTER, Mark  
; APPLICANT: JOHNSON, Kory  
; APPLICANT: HIGGS, Brandon  
; APPLICANT: CASTLE, Arthur  
; APPLICANT: ELASHOFF, Michael  
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5090US  
; CURRENT APPLICATION NUMBER: US/10/191,803  
; PRIOR FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,819  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/305,623  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: US 60/369,351  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: US 60/377,611  
; PRIOR FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 1140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 170  
; LENGTH: 4878  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM\_024400  
US-10-191-803-170

## Alignment Scores:

Pred. No.: 0 Length: 4878  
Score: 4292.00 Matches: 789  
Percent Similarity: 88.40% Conservatives: 57  
Best Local Similarity: 82.45% Mismatches: 97  
Query Match: 82.71% Indels: 14  
DB: 16 Gaps: 5

US-09-373-658C-2 (1-950) x US-10-191-803-170 (1-4878)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20  
Db 446 ATGGGGGACATCCAGCGGGCAGCGAAGTTTCGGAGCTCTCAGTCTGCACACATGCTGTTG 505  
QY 21 LeuLeuAlaAlaA-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37  
Db 506 CTACTCTCGTCCATACAAATGCTGTGTGTGGGGCGGCACACGCGCGCCCCACG 565  
QY 38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHis---GlyThr 56  
Db 566 GAGGACACGAGGAGCTGGTGTGCTCCCTCGTGTGAGCGCGCCCGGCCACGATTCRCC 625



Qy 57 ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuLeuArgProAspSer 76  
Db 626 ACACCTCTCGTCTGGAGCGCTTTGGTTCAGCAGCGTGCATCTGAASITGTCAGCCAGCAGC 685  
Qy 77 SerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgGlySerGlyThr 96  
Db 686 GGTTCCTTAGCGCTTGGCTTACCTTCAGCAGCGTGGCGCGAGCTCTGGTTCGAGGCA 745  
Qy 97 ProLeu-----ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGly 114  
Db 746 CAGCATCTGGACCCCACTGGGGAGCTGGCCCACTGCTTACTCTGGCAAGGTGAACGGT 805  
Qy 115 AspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeu 134  
Db 806 GACCCCAAGCTCCGCGCGCGCTCAGCCTCTGTGAAGGTGGCGGTGCTTCTACCTA 865  
Qy 135 LeuGlyGluAlaPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThr 153  
Db 866 CAAGCGGAGGAGTCTTCAITCAGCCAGCGCTGGGTGGCCAGCGCTGTCCTCCC 925  
Qy 154 AlaAlaProGlyGluLysProAlaProLeuGlnPheHisLeuLeuArgArgAsnArg 173  
Db 926 GCCCAACCGAAGGAGGAGTCAATCGCACTCCGCGGTTCACATCTCGAGCGGAAGCGG 985  
Qy 174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193  
Db 986 CGGGCGAGCGCGCGCGAAGTGGGTGTGTATGACGAGAGAGACCTGCCCAACC----- 1039  
Qy 194 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTyrSer 213  
Db 1040 -----AGCAACTCGGTTCGGAAGCGCAGAACCCCGGACCACTGGCCCT 1084  
Qy 214 ProGlnAspProAlaLeuGlnGlyValGlnProThrGlyThrGlySerIleArgLys 233  
Db 1085 CTGGGAGACCCCACTCTCTCAGGCGCGGGAAGCAACAGACCGAGGAGCTAAGGAAG 1144  
Qy 234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253  
Db 1145 AAGCGATTGTGTCCAGCCCGCTTATGTGGAACCACTGTCTGTGGTGTGACCACTCCATG 1204  
Qy 254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 273  
Db 1205 GCTGACTTCCACGCGCAGCGGTCTAAGCAATTAACCTTCTAACCCTGTCTCGGTGGCAGCC 1264  
Qy 274 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu 293  
Db 1265 AGATTTHCAAGACCCCAAGCATTAGGAAATCAATTAGTCTGTGGTGTGAAGATCTTG 1324  
Qy 294 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 313  
Db 1325 GTCATATATGAGGAGCAGACGAGCGGAGTACTTCCAAATGCGCTCTCAACCTTAGG 1384  
Qy 314 AsnPheCysAsnTyrGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333  
Db 1385 AATTTCGTAGTGGCAGAAACAGCAACAGCCCAAGTGCAGGATCCGGGATCCAGAGCACTAT 1444  
Qy 334 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 353  
Db 1445 GACACAGCGATTCTGTTCAACAGACAGGATTATGTGGCTCCCAACCTGTGACACTCTC 1504  
Qy 354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373  
Db 1505 GCGATGGCTGATGTGGAACTGATGTGACCCCAAGCAGAGAGTGTTCGGTCAATCGAAGAT 1564  
Qy 374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393  
Db 1565 GATGGTTTACAGCTTGCCTTCACACAGCCCATGAATGGGCCATGTGTTTAAACATGCCA 1624  
Qy 394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413  
Db 1625 CACGATGACGCAAGCACTGCGCCAGCTTTAATGGCGTGTGAGTGGGATTCCTCACTGATG 1684  
Qy 414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTyrSerProCysSerAlaTyrMet 433

Db 1685 GCCTCATGCTCTCCAGCTTGGACCAAGCCCTGTCTCTCTGAGTGCCTACATG 1744  
Qy 434 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 453  
Db 1745 GTCACATCATCTCTGACCAACCGCCATGGGGAATGTTTGTATGGACAAAGCGCAAGACCCA 1804  
Qy 454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAlaAsnArgGlnCysGlnPhe 473  
Db 1805 ATCAAGCTTCCATCTCATCTTCCCGTACTCTGTAGATGCCAACCGCCAGTGTCACTTT 1864  
Qy 474 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTyr 493  
Db 1865 ACCTTCGGGAGGAAATCAACGCACTCCCTGTATGTCAGCCAGCACATGTCAGTCCCTGTGG 1924  
Qy 494 CysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTyrAlaAsp 513  
Db 1925 TGCACTGGCACTCCCGTGGCTTACTGGGTGTCACCAACAAACACTTCCCTTGGGCAAT 1984  
Qy 514 GlyThrSerCysGlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLysThrAsp 533  
Db 1985 GGCACCACTGCGGAGAGGAAATGCTGTGTCAGCGCAAGTGTGTGAACAGACCCGAC 2044  
Qy 534 ArgLysHisPheAspThrProPheHisGlySerTyrGlyMetTyrGlyProTyrGlyAsp 553  
Db 2045 ATGAAGCACTTCTCTCTCTGTCATGGAGTGGGACCGTGGGACCATGGGGAGAC 2104  
Qy 554 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 573  
Db 2105 TGCTCAAGAACCTGTGGTGGAGGAGTTCATATACATAGAGAGATGTGACACCCGCTC 2164  
Qy 574 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593  
Db 2165 CCAAGAAACCGGGGAGTACTCGAAGGCAACGAGTCCGCTACAGGTCTCTGTAACTT 2224  
Qy 594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsn 613  
Db 2225 GAGACTGTCCACCAATACCGAAACATTCAGAGAGAGCATCCGAGGCGGCAAT 2284  
Qy 614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrPheProLysTyrAla 633  
Db 2285 GAGTTTCCAAAGCTTCTTTGGAAATGATCAACCGGTGGAATGACACCAAGTATGCT 2344  
Qy 634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653  
Db 2345 GCGGTCTCCGCAAGGACAGGTCAAGCTTACCTGGAGCCCAAGGCAATGGCTACTTC 2404  
Qy 654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673  
Db 2405 TTTGTTTTTACGCCAAGGTGTAGATGGCACTCCCTGTAGTCCAGACTCTACTCTGTGTC 2464  
Qy 674 CysValGlnGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 693  
Db 2465 TGTGTCAAGACAGTGTGTGAAGCTGGCTGTGATCGCATCATAGACTCCAAAGGAAG 2524  
Qy 694 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 713  
Db 2525 TTGCATAGTGTGGCGTTTGTGGAGGAATGGCTCCAGCTGCCAAGAAATATCAGGAACG 2584  
Qy 714 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 733  
Db 2585 GTCATAGTACAGACCTGGGTATCATGACATGTCTCAATTCCTGCTGGAGCCCAACAC 2644  
Qy 734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIle 753  
Db 2645 ATTGAAGTGAACATCTGTAATCCAGGGGATCCAGAAACAAATGSCAGCTTCTGGCTATT 2704  
Qy 754 LysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln 773  
Db 2705 AGACTGCAGATGCTACTTATTTCTGAATGGAAACTTCACTCTGTCCACTCTAGAGCAA 2764  
Qy 774 AspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg 793

2765	GACCTCACTCAAAAGTACTGTCTTAAGATACAGTGGTTCCTCACGACGATTTGGAAACA	2824
794	IleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsn	813
2825	ATCCGAGCGTTTATGTCCACTCAAAAGAACCCCTGACCATCCAGGTTCTTATGTGTGGCCCAT	2884
814	AlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPheAsn	833
2885	GCTCTCCGACCCAAATCAAGTACACTTATTTATGAAGAGAAGACGAGCCCTTCAC	2944
834	AlaIleProThrPheSerAlaTrpValIleGluLysGluTrpGlyGluCysSerLysSerCys	853
2945	GCTATTCCACATTTTCCGAGTGGGTGATTGAAGAGTGGGGGAGTGCTCCAAGACATGT	3004
854	GluLeuGlyTrpGlnArgGluValGluCysArgAspIleasnGlyGlnProAlaSer	873
3005	GGTTCGGTGTGCAGAGGAGTGGTGTAGAGTCAGAGACATTAATGGACACCCCTGCTCT	3064
874	GluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPro	893
3065	GAAATGTCCAAAGAGTGAAGCCAGCCAGTACCAGACCTGTGCACACCTCCTTGCACA	3124
894	GlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLys	913
3125	CGTTGGCAGTGGGGGATTTGTCACCATGCTCTTAAAACTTTGGGAAGGGTTATAAGAAG	3184
914	ArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAspPro	933
3185	AGAACCTTGAATGTCTGTCCCAATGAAGCGGTGTATTCAATGAGAGCTGTGATCCT	3244
934	LeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer	950
3245	TTGAAGAAACCAAGCATTACATTGACTTTGTCATCTACTGACACAGCTGCAGT	3295

## RESULT 15

US-09-445-023A-2  
Sequence 2, Application US/09445023A  
Patent No. US30030119167A1  
GENERAL INFORMATION:  
APPLICANT: Hirose, Kunitaka  
APPLICANT: Inoguchi, Ei-ji  
APPLICANT: Hakozaaki, Michinori  
APPLICANT: Ishioka, Keiko  
APPLICANT: Ishida, Yukako  
APPLICANT: Matsushima, Kouji  
APPLICANT: Kuno, Kouji  
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical composition and method of immunologically analyzing human ADAMTS

APPLICANT: Kuno, Kouji  
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

FILE REFERENCE: Q57092  
CURRENT APPLICATION NUMBER: US/09/445,023A

; CURRENT FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: JP 9-160422

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: patent in version 3.0
; SEC ID NO 2

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; SEQ ID NO 2
; LENGTH: 2184

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TYPE: DNA

; ORGANISM: Homo sapiens

**FEATURE:**

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; NAME/KEY: exon
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; LOCATION: (1) .. (2184)  
TTC-09-445-023A-2

US-09-445-023A-2

Alignment Scores:

Pred. No.:

Score:

Percent Similarity

Best Local Similarity Match.

Query Match:  
DB:

LB:

US-09-373-658C-2 (1-950} x US-09-445-023A-2 (1-2184)

Search completed: June 18, 2004, 23:44:17  
Job time : 1093.17 secs

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Qy	611	AlaHisAsnGluPheSerLysAlaSerPheGlySerClyProAlaValGluTrollePro	630
Db	1162	GCACACAAGAGTTTTCAAAAGCTTCCTTTGGGAGTGGGCTCGGTGGAAAGGATTCCC	1221
Qy	631	LysTyrAlaGlyValSerProLysAspArgCysLysLeuileCysGlnAlaLysGlylle	650
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Qy	651	GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer	670
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GenCore version 5.1.6  
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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	5230	98.9	3889	US-09-568-559-1	Sequence 1, Appl
3	5219	98.7	4858	US-09-392-184-1	Sequence 1, Appl
4	4262	80.6	3706	US-09-484-9703-58	Sequence 58, Appl
5	3922	74.2	2184	US-09-445-023A-2	Sequence 2, Appl
6	3652	69.1	2184	US-09-445-023A-13	Sequence 13, Appl
7	2271.5	43.0	3638	US-09-369-364A-8	Sequence 8, Appl
8	2165	40.9	3126	US-09-392-184-7	Sequence 7, Appl
9	2156	40.8	4192	US-09-122-126B-1	Sequence 1, Appl
10	2156	40.8	4192	US-09-634-286A-1	Sequence 1, Appl
11	1926.5	36.4	3250	US-09-122-126B-14	Sequence 14, Appl
12	1926.5	36.4	3250	US-09-634-286A-14	Sequence 14, Appl

13	1909.5	36.1	3002	4	US-09-369-364A-1	Sequence 1, Appl
14	1751.5	33.1	5804	4	US-09-369-364A-12	Sequence 12, Appl
15	1613	30.5	2625	4	US-09-369-364A-14	Sequence 14, Appl
16	1406	26.6	2114	4	US-09-130-491-7	Sequence 7, Appl
17	1333.5	25.2	5357	4	US-09-392-184-5	Sequence 5, Appl
18	1278.5	24.2	3675	4	US-09-930-872-3	Sequence 3, Appl
19	1278.5	24.2	4042	4	US-09-930-872-5	Sequence 5, Appl
20	1217	23.0	3218	4	US-09-369-364A-6	Sequence 6, Appl
21	1214.5	23.0	2727	4	US-09-963-791-1	Sequence 1, Appl
22	1203	22.8	3885	4	US-09-369-364A-16	Sequence 16, Appl
23	1151.5	21.8	2274	4	US-09-963-791-23	Sequence 23, Appl
24	1112	21.0	6592	4	US-09-491-522-1	Sequence 1, Appl
25	1096	20.7	4580	4	US-09-491-522-8	Sequence 8, Appl
26	1066.5	20.2	3160	4	US-09-963-791-25	Sequence 25, Appl
27	1040.5	19.7	1520	4	US-09-369-364A-3	Sequence 3, Appl
28	1038.5	19.6	2848	4	US-09-369-364A-4	Sequence 4, Appl
29	950.5	18.0	2450	4	US-09-491-522-2	Sequence 2, Appl
30	949.5	18.0	2450	4	US-09-491-522-9	Sequence 9, Appl
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33	712.5	13.5	739	4	US-09-369-364A-10	Sequence 10, Appl
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35	607.5	11.5	703	4	US-09-392-184-6	Sequence 6, Appl
36	595	11.3	5720	4	US-09-800-729-18	Sequence 18, Appl
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38	568.5	10.8	1803	4	US-09-369-364A-20	Sequence 20, Appl
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40	499	9.4	1407	4	US-09-963-791-5	Sequence 5, Appl
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43	439	8.3	852	4	US-09-800-729-54	Sequence 54, Appl
44	436	8.2	954	4	US-09-963-791-15	Sequence 15, Appl
45	433	8.2	3559	4	US-09-800-729-53	Sequence 53, Appl

## ALIGNMENTS

## RESULT 1

US-09-130-491-1  
; Sequence 1, Application US/09130491  
; Patent No. 6416974  
; GENERAL INFORMATION:

; APPLICANT: Goodgearl, Douglas A.  
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
; FILE REFERENCE: 09404/041001  
; CURRENT APPLICATION NUMBER: US/09/130,491  
; CURRENT FILING DATE: 1998-08-07  
; EARLIER APPLICATION NUMBER: US 60/058,108  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: US 60/054,961  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4676  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (460)...(3360)  
US-09-130-491-1

Alignment Scores:  
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Percent Similarity: 99.98%  
Best local similarity: 98.97%  
Query Match: 98.98%  
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Mismatches: 6  
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US-09-373-658C-126 (1-967) x US-09-130-491-1 (1-4676)

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Qy 841 PheValIysIysIysGlySerPheAsnAlaIleProThrPheSerAlaIleProValIle 860  
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Db 3340 TGCACAAATGCAGATGCAGT 3360

## RESULT 2

US-09-568-559-1  
; Sequence i, Application US/09568559  
; Patent No. 6549377  
; GENERAL INFORMATION:  
; APPLICANT: Klonowski, Paul  
; APPLICANT: Allard, John  
; APPLICANT: Heller, Renu  
; APPLICANT: Van Wart, Harold  
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid  
; FILE OF INVENTION: Compositions Encoding the Same  
; FILE REFERENCE: ROCH-002  
; CURRENT APPLICATION NUMBER: US/09/568,559  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: 60/133,343  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3889  
; TYPE: DNA  
; ORGANISM: human  
US-09-568-559-1

## Alignment Scores:

Pred. No.: 0 Length: 3889  
Score: 5230.00 Matches: 956  
Percent Similarity: 99.38% Conservative: 5  
Best Local Similarity: 98.86% Mismatches: 6  
Query Match: 98.92% Indels: 0  
DB: 4 Gaps: 0

US-09-373-658c-126 (1-967) x US-09-568-559-1 (1-3889)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyA-GATgLySLeuGlySerAspMetGlyVal 20  
Db 8 ATGACGAGATCTGTCCCGAGGGGTTCGAGAGGCGCAAGCTGGCAGCGCATCGGGGAAC 67  
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40  
Db 68 GCGAGCGGGCTCCGGGGGTCTCGAGAGCTTTGGGCCCGGTACCCACGCTGCTGCTCGCC 127  
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60  
Db 128 GCGGGCTACTGCGGCTGTGCGAGCGACTCGGGGCCCTCCGAGGAGGAGGAGAGCTA 187  
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80  
Db 188 GTGGTGGCGAGCTGGAGCGCGCCCGCGGACACGCGCCACCGCTCCGCTCGCACGCC 247  
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100  
Db 248 TTGACCCAGCAGCTGGATCTGAGCTGCGGCCCGCGCAGCAGCTTTTGGGCCCGGCTTC 307  
Qy 101 ThrLeuGlnAsnValGlyArgIysSerGlySerAspThrProLeuProGluThrAspLeu 120  
Db 308 ACCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGAGCGCCGCTTCGGAAACCGACCTG 367  
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140  
Db 368 GCGCACTGCTTCTACTCCGGCACCTGTAATGCGATGCCAGCTCGCTCGCTCGCCCTCAGC 427  
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160  
Db 428 CTCGCGAGGGGTGGCGGGCGCTTCTACTGCTGGGGAGGCGGTATTTTCATCCAGCGG 487  
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysProAlaPro 180  
Db 488 CTGCGCGCGCCAGGAGCGGCTTCGCCACCGCCGCCAGGAGGAGGAGGAGGAGGAGGAG 547  
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200  
Db 548 CTACAGTTCCACTCTCTCGCGCGGAATCGGCGGGCGAGCTCGCGGCGAGCTCGCGGGTTC 607  
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220  
Db 608 GTGGACGACGAGCCCGCGCGCTGGGAAAGCGGAGACCGAAGACGAGGACGAGGAGCT 667  
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaIleGluValGly 240  
Db 668 GAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727  
Qy 241 GlnProThrGlyThrGlySerIleArgIysLysArgPheValSerSerHisArgTyrVal 260  
Db 728 CAGCCCAAGAGACTGGAAGCATATAGAAGACGATTTGTCTCCAGTCACTCCGCTATGTG 787  
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuIysHis 280  
Db 788 GAAACCATGCTTGTGGCAGACAGCTCGATGGCAGAAATTCACCGGAGGTGCTTAAGCAT 847  
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrIysHisProSerIleArgAsn 300  
Db 848 TACCTTCTCAGCTTGTTCGTGGTGCAGCCAGATTTGTACAAACACCCAGCATTCGTAAT 907  
Qy 301 SerValSerLeuValValIysIleLeuValIleHisAspGluGlnIysGlyProGlu 320

908 TCAGTTAGCCTGGTGGTGAAGATCTTGGTTCATCCACGATGAACAGAAAGGGCCGGAA 967  
321 ValThrSerAsnAlaAlaLeuThrLeuAAspPheCysAsnTrpGlnLysGlnHisAsn 340  
968 GTGACCTCCAAATGCTCCCTTCACCTCGCGGAATCTTTGGCAACTGGCAGAGCAGACAAC 1027  
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaAlaLeuPheThrArgGlnAsp 360  
1028 CCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATCTTTTCCACGACAGGAC 1087  
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380  
1088 TTGATGGGGGCCAGACATGTGATCTCTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1147  
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400  
1148 CCGAGCAGAGAGTCTCCGTCATAGAGATGATGGTTTACAGCTGCCTTCCACACAGCC 1207  
401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420  
1208 CATGAATAGGCCACCTGTTTAAATGCGCACATGATGATGCAAGCAGTGTGCCAGCCTT 1267  
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440  
1268 AATGGTGTGAACACGATTTCCCAATGATGGCTCAATGCTTTCCAACTGACCAACAGC 1327  
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460  
1328 CAGCCTTGCTCTCTTGCAGTGCTACATGATATACATCATTTCTGGATTAATGGTCATGG 1387  
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480  
1388 GAAATGTTGATGACCAAGCTCAGATCCCATACAGCTCCAGGGGATCTCCCTGGCACC 1447  
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
1448 TCGTACGATGCCAACCGGAGTCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1507  
501 AsnAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyValLeuVal 520  
1508 GATCGACCGCAGCACATGTAGCACTTGTGTGTACCGGACCTCTGTGGGTGTGGTG 1567  
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540  
1568 TGTCAACCAACACATCTCCCGTGGCGGATGCCACAGCTGTGGAGAGGAAATGGTGT 1627  
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560  
1628 ATCAACGGCAAGTGTGTGAACAAACCCACAGAAAGCATTTTGATACGCTTTTCATGGA 1687  
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580  
1688 AGCTGGGGATGTGGGGGCTTGGGGAGACTGTTGAGAGAACTGTGGTGAGAGATCCAG 1747  
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600  
1748 TACACCATGAGGGAATGTACACACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGGC 1807  
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620  
1808 AAACGAGTGGCTACAGATCTCTGTACCTTGGAGACTGTCCAGACAAATTAATGGAAAAACC 1867  
621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640  
1868 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTCAAAAGCTTCTTTGGAGTGGG 1927  
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660  
1928 CTGCGGTGGATGGATCCCAAGTACGTGGCTCTCCAAAGACAGAGTGCAGGTC 1987  
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680  
1988 ATCTGCCAAGCCAAAGGCATGGCTACTTCTTCGTTTCCAGCCCAAGGTGTAGATGT 2047

681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700  
2048 ACTCCATGTAGCCAGATTCCACTCTCTGTGTGCAAGGACAGTGTGTAAAGCTGGT 2107  
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720  
2108 TGTGATCGCATCATAGACTCCAAAAGAAAGTTTGATAAATGTGTGTGTTTGGCGGAAAT 2167  
721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740  
2168 GGATCTACTTGTAAAAAAAATATCAGGATCAGTTACTAGTCAAAAACCTGGATATCATGAT 2227  
741 IleIleThrIleProThrGlyValaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760  
2228 ATCATCAAAATCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGAAACAGAGGGA 2287  
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780  
2288 TCCAGGAACAATGGCAGCTTTCTTCCCATCAAGCTGCTGATGGCACATATATTTCTAAT 2347  
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800  
2348 GGTGACTACACTTGTCCACCTTAGAGCAAGACATTAATGTACAAAGGTGTGTCTTGAGG 2407  
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820  
2408 TACAGCGCTCTCTCGCGCATTTGGAAGAAATTCGCACCTTTAGCCCTCTCAAGAGGCC 2467  
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840  
2468 TTGACCATCCAGTCTTACTGTGGGCAATCCCTTCGACCTAAANTAAATATACACCTAC 2527  
841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860  
2528 TTCGTAAGAAAGAAAGAGGAATCTTCAATGCTATTCCTCCACTTTTTCAGCATGGGTCAAT 2587  
861 GluGlnTrpDgLyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880  
2588 GAAAGATGGGGCGAATGTCTTAAGTCATGTGAATTTGGGTTGGCAGAGAGACTGGTAGAA 2647  
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900  
2648 TGCCGAGACATTAATGGACAGCTCTTCGAGTGTGCAAGGAAGTGAAGCCAGCCAGC 2707  
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920  
2708 ACCAGACCTTGTGCAGACCATCCCTGCCCGCAGTGGCAGCTGGGGGAGTGTGTCTCATGT 2767  
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940  
2768 TCTAAGACCTGTGGAGAGGTTACAAAAAAGAGCTTTGAAGTGTCTGTCCCATGATGGA 2827  
941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960  
2828 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTTCATAGATTT 2887  
961 CysThrMetAlaGluCysSer 967  
2888 TGCACATGGCAGAAATGCAGT 2908

## RESULT 3

US-09-392-184-1

; Sequence 1, Application US/09392184

; Patent No. 6395889

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: PROTEASE HOMOLOGS

; FILE REFERENCE: 5800-55

; CURRENT APPLICATION NUMBER: US/09/392,184

; CURRENT FILING DATE: 1999-09-09

; NUMBER OF SEQ ID NOS: 33

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A,T,C or G
US-09-392-184-1

Alignment Scores:
Pred. NO.: 0 Length: 4858
Score: 5219.00 Matches: 957
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 6
Query Match: 98.71% Indels: 1
DB: 4 Gaps: 0

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Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 514 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGGCCGTACCCACGCTGCTGCTGCC 573
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 574 GCGGCGTACTGTGGCGGTGTGGAGCGACTCGGGCGCCCTCCGAGGAGGACGAGACTA 633
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 634 GTGTGCGGAGCTGGAGCGCGCCCGGACACGCGACCGCGCTCCGCGCTCGACGCC 693
Qy 81 PheAspGlnGlnLeuAspValProProAspSerPheLeuAlaProGlyPhe 100
Db 694 TTTCACCGAGCTGTGATCTGGAGCTCGGGCCGACGAGACTTTTGGCGCCGCGCTTC 753
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
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Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
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Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 874 CTCTCGGAGGGCGTGGCGCGCCCTCTACTCTGTGGGGGAGCGGTATTTTCATCCAGCG 933
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 934 CTGCGCGCGCGCAGCGAGCGCTCGCCACCGCCCGCGGAGGAGAGCGCGCGACCA 993
Qy 181 LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
Db 994 CTACAGTTCCACTCTCTGCGCGGAGTCTGGCAGGCGGACGTAGCGGCGACGTGGCGGGTC 1053
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
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Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
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Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
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Db 1174 CAGCCACAGGAACCTGGAAGCATAGAAAGAGCGATTTGTCCAGTCAACCGCTATGTG 1233
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1234 GAAACCATGCTTGTGGCAGACAGTCGATGGCAGAATTCACGCGCAGTGTCTAAAGCAT 1293
Qy 281 TyrLeuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAs 300
Db 1294 TACTCTTCTCAACGTTGTTCGGTGGCAGCAGATGTACAAACACCCAGCATTCGTAA 1353
Qy 300 nSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProG 320
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Qy 320 uValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAs 340
Db 1414 AGTGACCTCCAATGCTCCCTCACTCTGGGAACTTTTGCACTGGCAGAGGAGCAACAA 1473
Qy 340 nProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAs 360
Db 1474 CCCACCCAGTGCAGCGGATGCAGAGCACTATGACACAGCAATTCCTTCCACGACAGGA 1533
Qy 360 pLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAs 380
Db 1534 CTGTGTGTGGTCCACAGACATGTATCTCTTGGGATGGCTGTGATGTTGGAACTGTGTGTA 1593
Qy 380 pProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAl 400
Db 1594 TCCAGCAGAGAGCTGCTCCGTATAGAGATGATGGTTTACAAAGCTGCTTCCACACAGC 1653
Qy 400 aHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLe 420
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Db 1714 TAAATGTGTGAACCAAGATTCACCATGATGGGTCTCATGCTTTCACCTGACCAACAG 1773
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Qy 460 yGluCysLeuMetAspIleProGlnAsnProIleGlnLeuProGlyAspLeuProGlyTh 480
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Qy 480 rSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPr 500
Db 1894 CTCTGACGATGCCAACCGGACGTGCCAGTTTACATTTGGGAGGACTCCAAACACTGCC 1953
Qy 500 oAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyValLeuVa 520
Db 1954 TGATGCGAGCAGCACATGTAGCACCTTGTGTGTACCGGCACCTCTGGTGGGTGTGCTGT 2013
Qy 520 lCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCy 540
Db 2014 GTGTCAAAACCAACATTTCCGTTGGCGGATGGCACCACTGTGGAGAGGAAATGGTG 2073
Qy 540 sIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisG 560
Db 2074 TATCAACGCGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTGATACGCTTTTCATGG 2133
Qy 560 ySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValG 580
Db 2134 AAGCTGGGAATGTGGGGCTTGGGGAGACTGTTCGAGAACCGTGGGTGGAGAGTCCA 2193
Qy 580 nTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyrCysGluG 600
Db 2194 GTACACGATGAGGAGATGTGACACCCAGCTCCCAAGAAATGGAGGAAGTACTGTGAAG 2253
Qy 600 yLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysTh 620
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Db 2254 CAAACGAGTGGCTACAGATCTGTAACTTGAGGACTGTCCAGACAATAATGMAAAAC 2313  
Qy rPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGI 640  
Db 2314 CTTTAGAGGAGACAAATGTGAGACACACACAGAGTTTTCAAAGCTTCTTTGGGAGTGG 2373  
Qy 640 yProAlaValGluTrrPileProLysTyrAlaGlyValSerProLysAspArgCysLysLe 660  
Db 2374 GCGTGGGGTGAATGGATTCCCAAGTACGCTGCGCTCTCACCAGAGAGAGAGTGAAGCT 2433  
Qy 660 uileCysGlnAlaLysGlyLeuGlyPhePheValLeuGlnProLysValValAspGI 680  
Db 2434 CATCTCCCAAGCCAAAGGCAATGGCTACTTCTTCGTTTGCAGCCCAAGTGTAGATGG 2493  
Qy 680 yThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGI 700  
Db 2494 TACTCCATGTAGCCAGATCCACCTCTGTCTGTGCAAGGACAGTGTAAAGCTGG 2553  
Qy 700 yCysAspArgIleileAspSerLysLysLysPheAspLysCysGlyValCysGlyValAs 720  
Db 2554 TTGTGATCGCATATAGACTCCAAAGAGAGTTTGATAATGTGGTGTTCGGGGGAAA 2613  
Qy 720 nGlySerThrCysLysLysLeuSerGlySerValThrSerAlaLysProGlyTyrHisAs 740  
Db 2614 TCGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAGAAACCTGGATATCATGA 2673  
Qy 740 pIleileThrIleProThrGlyAlaThrAsnIleGluValLysGlnAsnGlnArgGI 760  
Db 2674 TATCATCAAAATTCCAACTGGAGCCACCAACATCGAAGTGAACACGCGAAACGAGGGG 2733  
Qy 760 ySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAs 780  
Db 2734 ATCCAGGACAAATGGCAGCTTCTTCCCATCAAGCTGTGTGACACATATATCTTAA 2793  
Qy 780 nGlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyValValLeuAr 800  
Db 2794 TGGTGACTACACTTGTCCACCTTAGCAAGACATATATGACAAAGGTGTGTCTTGAG 2853  
Qy 800 gTyrSerGlySerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPr 820  
Db 2854 GTACAGGGCTCTCTCGCGCATGGAAAGAAATTCGACCTTTAGCCCTCTCAAGAGCC 2913  
Qy 820 oLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTy 840  
Db 2914 CTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTAATACACCTA 2973  
Qy 840 rPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrrValI 860  
Db 2974 CTTCTGTAAGAAGAGAGAGAAATCTTCAATGCTATCCCCACTTTTTCAGCATGGTCA 3033  
Qy 860 eGluGluTrrPlyGlyCysSerLysSerCysGluLeuGlyTrrPlnArgArgLeuValGI 880  
Db 3034 TGAAGAGTGGGGCAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGACTGGTAGA 3093  
Qy 880 uCysArgAspIleAsnGlyGlnProLysArgLysCysAlaLysGluValLysProAlaSe 900  
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Qy 900 rThrArgProCysAlaAspHisProCysProGlnTrrPlnLeuGlyGluTrrPserSerCy 920  
Db 3154 CACCAACCTTGTGCAGACATCCCTGCCAGTGGCAGTGGGGAGTGGTCAATCATG 3213  
Qy 920 sSerLysThrCysGlyLysGlyTrrLysLysThrSerLeuLysCysLeuSerHisAspGI 940  
Db 3214 TTCTAAGACTGTGGGAAGGGTTACAAAAAGAGAGCTTGAAGTGTCTTCCCATGATGG 3273  
Qy 940 yGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPh 960  
Db 3274 AGGGGTGTATCTCAGAGAGCTGTGATCTCTTAAAGAAACCTTAACATTTTCATAGACT 3333  
Qy 960 eCysThrMetAlaGluCysSer 967  
Db 3334 TTGCACATGGCAGATGTCAGT 3355

## RESULT 4

US-09-484-970B-58  
: Sequence 58, Application US/09484970B  
: Patent No. 6426186  
: GENERAL INFORMATION:  
: APPLICANT: Jones, Karen A.  
: APPLICANT: Volkmer, Wayne  
: APPLICANT: Walker, Michael G.  
: TITLE OF INVENTION: BONE REMODELING GENES  
: FILE REFERENCE: PB-0014 US  
: CURRENT APPLICATION NUMBER: US/09/484,970B  
: CURRENT FILING DATE: 2000-01-18  
: NUMBER OF SEQ ID NOS: 172  
: SOFTWARE: PERL Program  
: SEQ ID NO 58  
: LENGTH: 3706  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: misc feature  
: OTHER INFORMATION: Incyte ID No. 6426186 007074.1  
: LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3674, 3681  
: OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-58

## Alignment Scores:

Pred. No.: 0 Length: 3706  
Score: 4262.00 Matches: 772  
Percent Similarity: 99.36% Conservative: 1  
Best Local Similarity: 99.23% Mismatches: 4  
Query Match: 80.61% Indels: 1  
DB: 4 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-484-970B-58 (1-3706)

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Db 3 CAGGGCAGCTAGGCGGCACGTCGGGGTCTGTGGACGACGAGCCCGCCGACCTGGAAA 62  
Qy 211 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrrSer 230  
Db 63 GCGGAGACCGAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 122  
Qy 231 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 250  
Db 123 CCGCAGGACCCCGGCACTGCAAGGGCTAGGACAGCCACAGGAACTGGAAGCATAGAAG 182  
Qy 251 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 270  
Db 183 AAGCGATTTGTCTCCAGTCACCGCTATGTGGAAACCATGCTTGTGGCAGACCCAGT 242  
Qy 271 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 290  
Db 243 GCAGATTCACGGCAGTGGTCTTAAGCATTTACCTTCTTCAGTTGTTTTCGGTGGCACC 302  
Qy 291 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu 310  
Db 303 AGATTGTACAAACACCCCGCATTCGTAATTCAGTTAGCTGTGGTGGTGGTGAAGATCT 362  
Qy 311 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 330  
Db 363 GTCATCCAGATGAACAGAGGGGCGGAGTGAACCTCAATGCTGCCCTCCTCCTCGGG 422  
Qy 331 AsnPheCysAsnTrrPlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 350  
Db 423 AACTTTGCACCTGGCAGAACACGACACACCCAGTACCAGGATGCGAGACCTAT 482  
Qy 351 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 370  
Db 483 GACACGCAATTTCTTTTCCACAGACAGGACTTGTGTGGTGGTGGTGGTGGTGGTGGT 542

371 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 390  
Db GGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGGAAGCTGCTCCGCTCATAGAAGAT 602  
391 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 410  
Db GATGGTTTACAGCTGCCCTTCCACACAGCCCATGAATTTAGCCACCTGTTTACATGCCA 562  
411 HisAspAlaAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 430  
Db CATGATGATGCAAGCAGTGTGCCAGCCTTAATGTTGTGAACCCAGGATTCACACATGATG 722  
431 AlaSerMetLeuSerAsnLeuAspHisSerGlnProThrSerProCysSerGlyTyrMet 450  
Db GGTCTAATGCTTTCCAACTCCAGCCACAGCCCTGGTCTCTCTTGCAGTGCCTACATG 782  
451 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 470  
Db ATTACATCATCTCTGGTANTGTGATGGGGAATGTTTGTATGGACCAAGCTCAGATATCCC 842  
471 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 490  
Db ATACAGCTCCACAGCGCATCTCCCTGGCCACTCTGATGATGTCACCAACCGCAGTCCAGTTT 902  
491 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTyr 510  
Db ACAFTTGGGAGGACTCTCAAACTGCTGCCCGATGCGAGCGACACATGTAGCACCTTGTGG 962  
511 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProThrAlaAsp 530  
Db TGTATCCGGCACCTCTGTTGGGGTGTGCTGTGTCAAAACCAACACTTCCCGTGGCGGAT 1022  
531 GlyThrSerCysGlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLysAsnHis 550  
Db GGACCCAGCTGTGGAGAAGGGAATGTTGATCAACGGCAAGTGTGTGAACAAACCCGAC 1082  
551 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProThrGlyAsp 570  
Db AGAAGCAATTTGATACGCTTTTTCATGGAAGCTGGGGATGTTGGGGGCTTGGGAGAC 1142  
571 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgLysCysAspAsnProVal 590  
Db TGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACAGATGAGGGAATGTGAACACCCAGTC 1202  
591 ProLysAsnGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 610  
Db CCAAGGAATGGAGGAAGTACTGTGAAGGCAACGAGTGGCTACAGATCTGTATACCTT 1262  
611 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn 630  
Db GAGGACTGTCCAGACAATATGGAAGAAACCTTTAGAGAGGAACAATGTGAAGCACACAC 1322  
631 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrPheProLysTyrAla 650  
Db GAGTTTTCAAAAGCTTCTTTGGGAGTGGGCTCGGTGGATGGATTCGACAGTACCT 1382  
651 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 670  
Db GCGCTCTCACCAGGACAGGTGCAAGCTCATCTGCCAAGCAAGCAATGGCTACTTC 1442  
671 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 690  
Db TTCGTTTTGACGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTC 1502  
691 CysValGlnGlnGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 710  
Db TGTGTGCAGACAGCATGTGTAAAGCTGTTGTGATGTCATCATAGACTCCAAAAGAG 1562  
711 PheAspLysCysGlyValCysGlyGlnAsnGlySerThrCysLysLysIleSerGlySer 730  
Db TTTGATAAATGTTGTTGGGGGGAATGGAATCTACTTGTAAATAAATATATCAGATCA 1622  
731 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 750

1623 GTTACTAGTGCAAAACCTGGGATATCATGATATCATCAATTCCAATTCGAGCCACCAAC 1682  
751 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIle 770  
1683 ATCGAAGTGAACAGCGGAACAGAGGGGATCCAGGAAACAATGGGCAGCTTTCTTGCCAT 1742  
770 elysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln 790  
1743 CAAAGCTGCTGATGGCACATATTTCTTAATGGTGACTACACTTTGTCCACCTTAGACCA 1802  
790 nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg 810  
1803 AGACATTTATGTACAAAGTGTGTCTTGAGGTACAGCGGCTCTCTCGGGCATTTGGAAG 1862  
810 GileArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 830  
1863 AATTGCGAGCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCCTTACTTGGGCAA 1922  
830 nAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPheAs 850  
1923 TGCCCTTCGACCTAAATTAATACACTTCTGTAAGAGAGAGAGAGAAATCTTTCAA 1982  
850 nAlaIleProThrPheSerAlaIleTyrValIleGluTyrGlyGluCysSerLysSerCys 870  
1983 TGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCAATGTTCTAAGTCATG 2042  
870 sGluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSe 890  
2043 TGAATGGGTGGCAGAGAGACTGTGTAGAAATGCCGAGACATTAATGACAGCCTGCTTC 2102  
890 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 910  
2103 CGAGTGTGCAAGGAAGTGAAGCCAGCCAGCCAGCACCTTGTGACAGCATCCCTGCC 2162  
910 cGlnTyrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLysLys 930  
2163 CCAGTGGCAGCTGGGGAGTGTGTATGTTCTAAGACCTGTGGAGAGGTTTACAAAA 2222  
930 sThrSerLeuLysCysLysSerHisAspGlyGlyValLeuSerHisAspSerCysAspPr 950  
2223 AAGACCTTGAAGTGTCTCTCCATGATGGAGGGTGTATCTCATGAGAGCTGTGATCC 2282  
950 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967  
2283 TTTAAAGAAACCTAAACATTTTCATAGACTTTTGCACAATGGCAGAAATGCAGT 2334

RESULT 5  
US-09-445-023A-2  
; Sequence 2, Application US/09445023A  
; Patent No. 6565858  
; GENERAL INFORMATION:  
; APPLICANT: Hirose, Kunitaka  
; APPLICANT: Inoguchi, Eiji  
; APPLICANT: Hakozaeki, Michinori  
; APPLICANT: Ishioaka, Keiko  
; APPLICANT: Ishida, Yukako  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Kuno, Kouji  
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical  
; FILE REFERENCE: Q57092  
; CURRENT APPLICATION NUMBER: US/09/445,023A  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: JP 9-160422  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 2184  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

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; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:
Pred. No.: 0          Length: 2184
Score: 3922.00       Matches: 707
Percent Similarity: 98.89%   Conservatives: 5
Best Local Similarity: 98.19%   Mismatches: 8
Query Match: 74.18%          Indels: 0
DB: 4                      Gaps: 0

US-09-373-658c-126 (1-967) x US-09-445-023A-2 (1-2184)

QY 248  l l e a r g l y s i a r g p h e v a l s e r s e r h i s a r g t y r v a l g l u t h r m e t l e u v a l a l a s p 267
DB 22  c r t a g a a a g a a g c g a t t t g t g c c a g c c c c c c g t a t g t g g a a a c c a t g c t t g t g c a g a c 81

QY 268  g i n s e r m e t a l a g l u p h e i s g l y s e r g l y l e u l y s h i s t y r l e u l e u t h r l e u p h e s e r 287
DB 82  c a g t c g a t g c c a g a n t t c c a c g c c a g t g g t c t a a a g c a t t a c c t t c t c a o g t t g t t t c g 141

QY 288  v a l l a l a a r g l e u t y r l y s h i s p r o s e r i l e a r g a s n s e r v a l s e r l e u v a l v a l 307
DB 142  g f g g c a g c a g a n t t g t a c a a a c a c c c c a g c a t t c g t a a t t c a g t t a g c t t g g t g g t g 201

QY 308  l y s i l e l e u v a l l e i h i s a s p g l u g l n l y s g l y p r o g l u v a l t h r s e r a s n a l a l a l e u 327
DB 202  a n g a t c t t g t c a t c c a c a t g a a c a g a a g g g c c g a g t a g c c t c c a a t g c t c c c t c 261

QY 328  t h r l e u a r g a s n p h e c y a s n t r p g l n l y s g l n h i s a s n p r o s e r a s p a r g a s p a l a 347
DB 262  a c t c t g c g g a a c t t t t g c a a c t g g c a g a c a g c a c a c c a c c a g t g a c c g g a t g c a 321

QY 348  g l u h i s t y r a s p t h r a l a i l e u p h e t h r a s g l n a s p l e u c y a s g l y s e r g l n t h r c y s 367
DB 322  g a g c a t a t g a c a c a g c a n t t c t t t t c a c a g a c a g a c t t g t g t g g g t c c a g a c a t g t 381

QY 368  a s p t h r l e u g l y m e t a l a s p v a l g l y t h r v a l c y s a s p p r o s e r a r g s e r c y s s e r v a l 387
DB 382  g a t a c t c t t g g a t g c t g a t g t g a a c t g t g t g a t c c g a g c a g a g c t c c g t c 441

QY 388  i l e g l u a s p a s p g l y e u c l n a l a p h e t h r t h r a l a h i s g l u l e u c l y h i s v a l p h e 407
DB 442  a t a g a a g a t g t g t t t a c a g c t g c t t t c a c a g a c c c a t g a a t t a g g c c a c g t g t t 501

QY 408  a s n m e t p r o h i s a s p a l a l y s g l n c y s a l a s e r l e u a s n g l y v a l a s n g l n a s p s e r 427
DB 502  a a c a t g c c a c a t g a t g a t g c a a a g c a g t g t g c c a g c t t a a t g g t g t g a a c c a g a t t c c 561

QY 428  h i s m e t m e t a l a s e r m e t l e u s e r a s n l e u a s p h i s s e r g l n p r o t r p s e r p r o c y s s e r 447
DB 562  c a c a t g a t g c c t c a a t g c t t t c c a a c t t g g a c c a c a g c c a g c c t t g g t c t c t t t g c a g t 621

QY 448  g l y t y r m e t i l e t h r s e r p h e l e u a s p a s n g l y h i s g l y g l u c y s l e u m e t a s p l y s p r o 467
DB 622  g c t a c a t g a t t a c a t c a t t c t g a n a t a t g t c a t t g g g a a t g t t g a t g a c a a g c c t 681

QY 468  g l n a s n p r o i l e g l e u p r o g l y a s p l e u p r o g l y t h r s e r t y r a s p a l a a s n a r g g l n 487
DB 682  c a g a a t c c c a t a c a g c t c c c a g c g a t c t c c c t g c c a c c t t g t a c g a t g c c a a c c g g c a g 741

QY 488  c y s g l n p h e t h r p h e g l y g l u a s p s e r l y s h i s c y s p r o a s p a l a a l a s e r t h r c y s s e r 507
DB 742  t g c c a g t t t a c a t t t t g g g a g a c t c c a a a c a c t g c c c c g a t g c a g c c a g a c a t g a t a g c 801

QY 508  t h r l e u t r p c y e t h r g l y t h r s e r g l y g l y v a l l e u v a l c y s g l n t h r l y s h i s p h e p r o 527
DB 802  a c c t t g t g g t a c c g c a c c t c t g t g g g g t g t g t g t g t g t g t g t g t g t g t g t g t g t g t g t g 861

QY 528  t r o p a l a s p g l y t h r s e r c y s g l y g l u g l y s t r p c y s i l e a s n g l y l y s c y s v a l a s n 547
DB 862  t g g c g g a t g g c c a c c a g c t g t g g a a g g a a a t g g t g t a t c a a c g c a a g t g t g t g a a c 921

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QY 548  l y s a s n h i s a r g l y s h i s p h e a s p t h r p r o p h e i s g l y s e r t r p g l y m e t t r p g l y p r o 567
DB 922  a a a a c c a c a g a a g c a t t t t g a t a c g c c t t t t c a t g a a g c t g g g a c c a t t g g g a c c g 981

QY 568  t r p g l y a s p c y s s e r a r g t h r c y s g l y g l y v a l g l n t y r t h r m e t a r g g l u c y s a s p 587
DB 982  t g g g a g a c t g t t c g a g a a c g t g c g t g g a g g a g t c c a g t a c a g a t g a g g a a t g t g a c 1041

QY 588  a s n p r o v a l p r o l y s a s n g l y g l y l y s t y r c y s g l u g l y s a r g v a l a r g t y r a r g s e r 607
DB 1042  a a c c a g t c c c a a a g a a t t g g a g g a g a c t g t g t a a g g c a a a c a g a t g c g t a c a g a t c c 1101

QY 608  c y s a s n l e u g l u a s p c y s p r o a s p a s n a s n g l y l y s t h r p h e a r g g l u g l u g l c y s g l u 627
DB 1102  t g t a a c c t t g a g a c t g t c c a g a c a a t a a t g a a a a a c c t t t a c a g a g a c a a t a t g t g a a 1161

QY 628  a l a h i s a n g l u p h e s e r l y s a l a s e r p h e c y s e r g l y s e r g l y p r o l a v a l g l u t r p l e p r o 647
DB 1162  g c a c a c a c a g a g t t t c a a a a g c t t c c t t t g g g a g t g g c c t g c g t g g a a t g a a t t c c c 1221

QY 648  l y s t y r a l a g l y v a l s e r p r o l y s a s p a r g c y s l y s l e u r l e c y s g l n a l a l y s g l y l e 667
DB 1222  a a g t a c c g t g c g t c t c a c c a a g a c a g t g c a a g c t c a t c t g c c a a g c c a a a g c a t t 1281

QY 668  g l y t y r p h e v a l l e u g l n p r o l y s v a l v a l a s p g l y t h r p r o c y s s e r p r o a s p s e r 687
DB 1282  g g c t a c t t c t t c g t t t t g c a c c c c a a g g t t g t t g a t g s t a c t c c a t g t a g c c a g a t t c c 1341

QY 688  t h r s e r v a l c y s v a l g l n g l y g l n c y s v a l l y s a l a g l y c y s a s p a r g l e i l e a s p s e r 707
DB 1342  a c c t c t g t g t g t g c a a g a c a g t g t g t a a a g c t g t t g t g a t c c g a t c c a t a t a g a t c c 1401

QY 708  l y s l y s l y s p h e a s p l y s c y s g l y v a l c y s g l y a s n g l y s e r t h r c y s l y s l y l e 727
DB 1402  a a a a a a a g t t t g a t a a a t g t g t t t t g c g g g g a a a t g g a t c t a c t t g t a a a a a a a t a 1461

QY 728  s e r g l y s e r v a l t h r s e r a l a l y s p r o g l y t y r h i s a p l e i l e t h r l e p r o t h r g l y 747
DB 1462  t c a g a t c a g t a c t a g t g c a a a a c c t g g a t a t c a t a t a t c g t a c a a t t c c a a c t t g g a 1521

QY 748  a l a t h r a s n i l e g l u v a l l y s g l n a r g a s n g l n a r g g l y s e r a r g a s n a s n g l y s e r p h e 767
DB 1522  g c c a c c a c a t c c a g a t g a a c a c a g a g g g a t c c a g a c a a c a a t g c c a g c a t t 1581

QY 768  l e u a l a l e l y s a l a l a s p g l y t h r t y r l e u a s n g l y a s p t y r t h r l e u s e r t h r 787
DB 1582  c t t g c c a t c a a a g c t g c t g a t g g c a c a t a t a t t c t t a a t g t g a c t a c a c t t t g t c c a c c 1641

QY 788  l e u g l u g l n a s p i l e m e t t y r l y s g l y v a l l e u a r g t y r s e r g l y s e r s e r a l a l a 807
DB 1642  t t a g a c a a g a c a t a t g t a c a a a g g t g t g t c t t g a g g t a c a g c g c t c c t c t c t g c g c a 1701

QY 808  l e u g l u a r g l e a r g s e r p h e s e r p r o l e u l y s g l u p r o l e u t h r l l e g l n v a l l e u t h r 827
DB 1702  t t g a a a g a a t t c g a g c t t t a g c c c t c t c a a a g a g c c c t t g a c c a t c c a g g t t c t t a c t 1761

QY 828  v a l g l y a s n a l a l e u a r g p r o l y s l e l y s t y r t h r t y r p h e v a l l y s l y s l y s g l u 847
DB 1762  g t g g c a a t g c c c t t c g a c c t a a a n t t a a a t a c a c c t a c t t c g t a a a g a g a g a g a g a 1821

QY 848  s e r p h e a s n a l a l e p r o t h r p h e s e r a l a t r p v a l l e g l u g l u t r p g l y g l u c y s e r 867
DB 1822  t c t t t c a a t g c t a t c c c a c t t t t t c a g c a t g g g t c a t t g a a g a g t g g g c g a a t g t t c t 1881

QY 868  l y s s e r c y s g l u l e u g l y t r p g l n a r g a r g l e u v a l g l u c y s a r g a s p i l e a s n g l y g l n 887
DB 1882  a a g t c a t t g t g a a t t g g g t g c a g a g a g a c t g t g a a t t g c c a g a c a t t a t t a t t g a c a g 1941

QY 888  p r o a l a s e r g l u c y s a l a l y s g l u v a l l y s p r o a l a s e r t h r a r g p r o c y s a l a a s p h i s 907
DB 1942  c c t c t t c c g a g t g t g c a a a g a a g t g a a g c c a g c a c c a g a c c t t g t g c a g a c c a t 2001

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Qy 908 ProCysProGlnThrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGly 927  
Db 2002 CCCTGCCCCAGTGGCAGCTGGGGAGTGGTTCATCATGTTCTAAGACCTGTGGAGGGT 2061  
Qy 928 TyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSer 947  
Db 2062 TACAAAAAAGAGCTTGAAGTGTCTGTCCTCCATGATGGAGGGGTATTCTCATGAGAGC 2121  
Qy 948 CysAspProLeuLysLysProLysHisPheLeuLeuAspPheCysThrMetAlaGluCysSer 967  
Db 2122 TGTGATCCCTTTAAAGAAACCTAAACATTTTCATAGACTTTTGCACACTGCACAGTGCAGT 2181  
RESULT 6  
US-09-445-023A-13  
; Sequence 13, Application US/09445023A  
; Patent No. 6563858  
; GENERAL INFORMATION:  
; APPLICANT: Hirose, Kunitaka  
; APPLICANT: Inoguchi, Eiji  
; APPLICANT: Hakozaaki, Michinori  
; APPLICANT: Ishioaka, Keiko  
; APPLICANT: Ishida, Yukako  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Kuno, Kouji  
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical  
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS  
; FILE REFERENCE: 057092  
; CURRENT APPLICATION NUMBER: US/09/445,023A  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: JP 9-160422  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 2184  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (11..(2184)  
US-09-445-023A-13

Alignment Scores:  
Pred. No.: 0 Length: 2184  
Score: 3652.00 Matches: 646  
Percent Similarity: 94.77% Conservative: 43  
Best Local Similarity: 88.86% Mismatches: 38  
Query Match: 69.08% Indels: 0  
DB: 4 Gaps: 0  
US-09-373-658C-126 (1-967) x US-09-445-023A-13 (1-2184)

Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260  
Db 1 AAGCCATCAGGACCCAGGAGCATTAAGGAGAGCGGATTTGTCCAGCCCCCGTTATGTG 60  
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280  
Db 61 GAAACCAATGCTGTAGTGCACCGAGTCCATGCGCGACTTCCACGCGACGCGTCTAAAGCAT 120  
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300  
Db 121 TACCTTCAACCCCTGTCTCTCGTGGAGCAGCGTTTACAAAGCATCCAGCATTAGGAAT 180  
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320  
Db 181 TCAATTAGCCCTGGTGGTGGTGGAGATCTTGCTCATATACGAGGAGCAGAGGACAGAA 240  
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340  
Db 241 GTTACCTCCCAATGAGCTCTCACCCCTTCGGAAATTTCTGACAGTGGCAGAAACCAAC 300  
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360

Db 301 AGCCCCAGTGACCGGATCCAGAGCACTATGACACTGCAATTCGTTCACCACACAGGAT 360  
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380  
Db 361 TTATGTGGTCCACACACGCTGACACTCTCGGAATGCGAGATCTTGGAAACCGTATGTGAC 420  
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400  
Db 421 CCAGCAGAGAGTGTCTCATGATAGAGATGATGGTTGCAAGCTGCTTCACACAGGCC 480  
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420  
Db 481 CATGAATTGGCCCATGTGTTAAACATGCCGACGATGATGAAGCACGTGTGCCAGCTTG 540  
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440  
Db 541 AATGGTGTGATGGCGGATCTCATGATGGGCTCGATGCTCTCCAGCTTAGACCATAGC 600  
Qy 441 GlnProTyrSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460  
Db 601 CAGCCCTGGTCCACTTGCAGTGCCTACATGGTTCACGTCTCTCTAGATATGACACGGG 660  
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480  
Db 661 GAATGTTTTCATGGACAAAGCCAGAAATCCAAATCAAGCTCCCTTCTGATCTTCCCGGTACC 720  
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
Db 721 TTGTAGATGCCAACCCAGGTGTGAGTTTACATTCGGAGAGAAATCCAAAGCATGCCCC 780  
Qy 501 AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyValLeuVal 520  
Db 781 GATGAGCCAGCACATGTTACTACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 521 CysGlnThrLysHisPheProThrAlaAspGlyThrSerCysGlyGluGlyLysTyrCys 540  
Db 841 TGCCAAACAAACACATTCCTTGGGAGATGGCAGCTGTGGAGAGGAGGAGTGGTGT 900  
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560  
Db 901 GTCAGTGGCAAGTGGTGGACAGACAGACATGAAGCATTTGCTACTCTCTGTTATGGA 960  
Qy 561 SerTyrGlyMetTyrGlyProTyrGlyAspCysSerArgThrCysGlyGlyValGln 580  
Db 961 AGCTGGGGCCATGGGGACCGTGGGAGACTGCTCAAGAACCTGTGGTGGTGGAGTTCAA 1020  
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyrCysGluGly 600  
Db 1021 TACCAATGAGAGATGTGACAAACCCAGTCCCAAGAACGGAGGAGTACTGTGAGGC 1080  
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620  
Db 1081 AAACGAGTCCGCTACAGTCTCTTAACATCGAGGACTGTCCAGACAAATTAACGAAACAG 1140  
Qy 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640  
Db 1141 TTCAGAGAGGAGGAGTGGCAGGCGGACATGATGTTTCCAAAGCTTCCTTTTGGAAAGAG 1200  
Qy 641 ProAlaValGluTyrIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660  
Db 1201 CCCACTGTAGTGGACACCCCAAGTACGCGCGCTCTGCCAAAGGACAGGTGCAAGCTC 1260  
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680  
Db 1261 ACCTGTGAAGCCAAAGGCAATGGCTACTTTTTCGCTTACAGCCCAAGGTGTGAGTGGC 1320  
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700  
Db 1321 ACTCCCTGTAGTCCAGACTCTTACTCTGTCTGTGTGCAAGGCGAGTGTGTGAAGCTGCG 1380  
Qy 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720



Qy	255	SerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHis	274
Db	968	TCCGAGGCTCGCTTCGTGGAAACACTTCTGGTGGCTGATCGTCCATGGCTGCTTCTAT	1027
Qy	275	GlySerGlyLeuLysHisFyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLys	294
Db	1028	GGGACCGACCTGCAGAACCACTCTCACGGTGATGTCATGGCAGCCCGAATCTACAAG	1087
Qy	295	HisProSerIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAsp	314
Db	1088	CACCCGAGCATCAGAAATCCGTCACACTTGTGGTGTGAAAGTCTTAATAGTGGAAAAA	1147
Qy	315	GluGlnLysGlyProGluHuValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsn	334
Db	1148	GAAGAATGGGGCCCCGGAGGTGCCAGACAGGGGGCTCACATGCCCACTTCTGCGAGC	1207
Qy	335	TrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIle	354
Db	1208	TGGCAACGGGGTTTCAACAAGCCCACTGACCGCCACCCGGAGCACTATGACACTGCCCATC	1267
Qy	355	LeuPheThrArgGlnAspLeuCysGly---SerGlnThrCysAspThrLeuGlyMetAla	373
Db	1268	TTGTTCACCAACAGAACTTCTGTGGAAAGGAGAGCAGGTGTGACACCTTGGGGGATGGCA	1327
Qy	374	AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeu	393
Db	1328	GACGTTGGCAACATCTGTGACCCCGACAAGAGCTGCTCAGTGATCAAGATGAGGAGCTG	1387
Qy	394	GlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp	413
Db	1388	CAGGCACCTTACACCTCGGCCCATAGCTAGCTAGGCACTGCTTCAGCATGCCCATGATGAT	1447
Qy	414	AlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMet	433
Db	1448	TCTAAGCCCTGTGTGAGATTGTTGGGCCCATCGGGCAAGTATCCACATGATGGCGCCATTC	1507
Qy	434	LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSer	453
Db	1508	TTCATCCACGTGAACAAGACGCTGCCCTCTGCTCCCTGCAGTGTCTACTCTACCTCACAGAG	1567
Qy	454	PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu	473
Db	1568	CTCCGTGATGATGTGTCCAGAGATGTCTCTGTGATGCCCCACCTCGGTTCTGCCCTC	1627
Qy	474	ProGlyAspLeuProGly-----ThrSerTyrAspAlaAsnArgGlnCysGlnPheThr	491
Db	1628	CCCAAGCCCTCCCGGGCCACAGCACCTCTACAGCTGGACAGCAGTSCAAGCAGATC	1687
Qy	492	PheGlyLysAspSerLysHisCysProAspAlaAla-----SerThrCysSerThrLeu	509
Db	1688	TTTGGGCGCTGATTTCGACACTGCCCCACACCTCTGTGGAGGACATCTGTGTCCAGCTC	1747
Qy	510	TrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHis-----PhePro	527
Db	1748	TGTGCCCGCTCATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1807
Qy	528	TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn	547
Db	1808	TGGGCTCATGTGTACACCTGTGGCCCTCGGGCCCTGTGCCCTGGATGTGTGTGTGTGTGT	1867
Qy	548	LysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro	567
Db	1868	AAGAGAGATGTGGAGATCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1927
Qy	568	TrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAsp	587
Db	1928	TGGGGCAATGTTCTCCGCACTGT	1987
Qy	588	AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer	607
Db	1988	AATCCAAATGCTCAGATGGAGGAAGATTGCTGGGTGAAAGAGTCAAGTACCAATCA	2047
Qy	608	CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnGlnCysGlu	627

[illegible]

RESULT B  
US-09-392-184-7/c  
; Sequence 7, Application US/09392184  
; Patent No. 6395889  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.



GENERAL INFORMATION:			US-09-373-658C-126 (1-967) x US-09-122-126B-1 (1-4192)		
APPLICANT: Bristol-Myers Squibb Company			7 GluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArgAlaProGly 26		
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES			432 GAGGGCGTTGGCAGGGCCGCTGCTGT-GGGAGGCCAACCTGCTCTCTCCCAATTG 490		
FILE REFERENCE: DM6909			27 SerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaLeuLeuAlaVal 46		
CURRENT APPLICATION NUMBER: US/09/122.126B			491 TGCGCTCTCTGGCTG-GTGTGGCTGCTCTGCTACTGCTGCTGCTCTCTCTCTGCCC--- 546		
CURRENT FILING DATE: 1998-07-24			47 SerAspAlaLeuGlyArgProSerGluGluAspGluLeuValValProGluLeu--- 65		
NUMBER OF SEQ ID NOS: 21			547 TCAGCCCGCTGGCAGCCCTCTCCCGGAGGAGGAGTCGTGTTTCCAGAGAGCTC 506		
SOFTWARE: PatentIn version 3.0			66 -----GluArgValProGlyHisGlyThr---ThrArgLeu-----ArgLeuHisAla 80		
SEQ ID NO 1			607 AACGCAGCGCTCTGCTGCTGGCTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCGGCC 666		
LENGTH: 4192			81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100		
TYPE: DNA			667 TTTGGGAGAGCGCTCTACTAGCTGAGCTGAGCAGGAGACTCCGCTGTCAGCTCAGGGGCTG 726		
ORGANISM: Homo sapiens			101 ThrLeuGlnAsnValGlyArgLys-----SerGlySerAspThrProLeuPro 116		
FEATURE:			727 ACGTGTACGTACTCTGGCGCAGCGCTGAGCTGCTGGGTGGAGCAGAG-----CCT 777		
NAME/KEY: CDS			117 GluThrAspLeuAlaHisCysPheThrValAsnGlyThrValAsnGlyAspProSerAla 136		
LOCATION: (406) .. (2916)			778 GGCACC-----TACCTGACTGGCACCACATCATGGAGATCCGGAGTCGGTG 822		
US-09-122-126B-1			137 AlaAlaLeuSerLeuCysGluGly---ValArgGlyAlaPheThrLeuLeuGlyGluAla 155		
Alignment Scores:			823 GCATCTCTGCACTGGGATGGGGAGCCCTCTGTAGCGCTGTACATATCGGGGGCTGAA 882		
Pred. No.:	9,54e-185	Length:	156 TyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlu 175		
Score:	2156.00	Matches:	883 CTCACCTCCAGCCCTGGAGGGAGGACCCCTAACTCTGCT---GGGGAGCTGGGGCT 939		
Percent Similarity:	60.55%	Conservative:	176 LysProProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGly 195		
Best Local Similarity:	45.87%	Mismatches:	940 -----CACATCTACCGCCGGAAG----- 957		
Query Match:	40.78%	Indels:	196 GlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAsp 215		
DB:	4	Gaps:	957 ----- 957		
US-09-373-658C-126 (1-967) x US-09-122-126B-1 (1-4192)			216 GluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAla 235		
656 AspArgCysLysLeuLeuCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnPro 675					
1464 GACCGCTGCAAGTTGTTCTGCGAGCCCGGGAGGAGCGAGTTCAAAAGTGTTCGAGGCC 1405					
676 LysValValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGln 695					
1404 AAGGTGATTGATGGCACCCTGTGTGGCCAGAAACACTGGCCACTGTGTGCTCGTGGCCAG 1345					
696 CysValLysAlaGlyCysAspArgIleLeuAspSerLysLysValPheAspLysCysGly 715					
1344 TGTGTCAAGCCCGCTGTGACCATGTGGTGAGCTGCTCGGAAGCTGGACAAATGGCG 1285					
716 ValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLys 735					
1284 GTGTGTGGGGGAAAGGCAACTCTCTGAGCAAGAGTCTCGGGTCTCTACCCGCCCAAT 1225					
736 ProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGln 755					
1224 TATGGCTACAATGACATTGTCACCATCCAGCTGGTGCCACTTAATATTGACGTGAGCAG 1165					
756 ArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGly 775					
1164 CGGAGCCACCGGCTGTGCAGAAACGATGGGAACACTACCTGGCGCTGAAGACGGCTGATGG 1105					
776 ThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGluAspIleMetTyrLys 795					
1104 CAGTACCTGCTCAACGGCAACCTGCGCATCTGCGCTAGCAGCAATCTTGTGAG 1045					
796 GlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSer 815					
1044 GGGACCATCTGAGGTACAGCGCTCATCGCCACCTGGAGCGCTGCGAGAGCTTCGG 985					
816 ProLeuLysGluProLeuThrIleGlnValLeuThrVal---GlyAsnAlaLeuArgPro 834					
984 CCCTTGCCAGAGCTCTGACGTGACGTCCTGACAGTCCCTGGCGAGGTCTTCCGCCCA 925					
835 LysIleLysTyrThrTyrPheVal-----LysLys 844					
924 AAGTCAATATACCTTCTTGTTCCTAATGAGCTGGACTTTAGCATGCGAGAGCAGCA 865					
845 LysLysGluSerPheAsnAlaIle---ProThrPheSerAla---TrpValIleGluGlu 862					
864 GAGAGCAACCAACCAACATCATCCAGCGCTGCTCCAGCGACAGTGGGTGCTGGGGAG 805					
863 TrpGlyGlyCysSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGluCysArg 882					
804 TGTCTGAGTGTCTAGCACTCGGGGCGGCTGGCAGAGGGAACCTGTAGAGTGCAG 745					
883 AspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArg 902					
744 GACCCCTCGGCGAGGCCCTGCGACCTGCAACAGAGCTCTGAACCCCGAGGATGCCAAG 685					
903 ProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSer---CysSe 921					
684 CCCTGCAAGAGCCAGCTGTGCCCCCTGTGATTCAGGGGGGAGGGGCCAGTCTGTGCTC 625					
921 xLysThrCysGlyLysGlyTyrLysLysThrSerLeuLys----- 934					
624 CTGACATGCGGT-----ACTGAGGTGCAGACAGGGTCTCCACTGTGT 580					
935 -----CysLeuSerHisAspGlyValLeuSerHisAspSerCysAspProLeuLys 952					
579 GACTGGGTCCCTTGGCCATAT-CAAGGACAGCAGCGGCCACCCAGGCGCTC---CCATTGCC 524					
952 sLysProLysHisPheIleAspPheCysThr 962					
523 GCAACCC-----CTCCAGTACTGCACA 502					
RESULT 9					
US-09-122-126B-1					
Sequence 1, Application US/09122126B					
Patent No. 6451575					







QY	535	GlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPhe	554
DB	1891	GGGCCCCGACAGCGCTGCATGGGTGGTGGCTCCACATGCACCGACTCCAGACTTC	1950
QY	555	AspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThr	574
DB	1951	AATATTCCACAGAGCTGGTGGCTGGGTCCCTGGGACCATTGGGGTCACTGCTCTCGGACC	2010
QY	575	CysGlyGlyValGlnTrpThrMetArgGluCysAspAsnProValProTyrAsnGly	594
DB	2011	TGTGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACGAGGCTGTGCCCGGAATGGT	2070
QY	595	GlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysPro	614
DB	2071	GGCAAGTACTGTGAGGCGCCCGCTACCCGCTCTCGCTCTCGCAACACTGAGGACTGCCCA	2130
QY	615	AspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLys	634
DB	2131	ACTGGCTCAGCCCTGACCTTTCGCGAGGACGAGTGTCTCCTACACCAACCACCGAC	2190
QY	635	AlaSerPheGlySerGlyProAla---ValGlnTrpIleProLysTrpAlaGlyValSer	653
DB	2191	CTC---TTCAAGAGCTTCCAGGCGCCCATGAGTGGGTTCCTCGCTACAGCGGTGGCC	2247
QY	654	ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu	673
DB	2248	CCCAGAACAGTCAAACTCACCTGCAGGCCCGGCGCACTGGGCTACTACTATGTGCTG	2307
QY	674	GlnProLysValAlaAspGlyThrProCysSerProAspSerThrSerValCysValGln	693
DB	2308	GAGCCAGGTTGGTAGATGGACCCCTGTTCCTCCGACAGCTCTCTCGTCTGTGTCCAG	2367
QY	694	GlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLys	713
DB	2368	GGCCGATGCATCCATGCTGCTGTGATCGCATCATTTGGCTCCAAGAAGATTGCACAG	2427
QY	714	CysGlyValCysGlyGlyAsnGlySerThrCysLysLysLysIleSerGlySerValThrSer	733
DB	2428	TGCATGTGTGCGAGGGACGGTTCGTGTGCAGCAGCAGTCAGGCTCCTTCACGAAA	2487
QY	734	AlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluVal	753
DB	2488	TTCAAGTACGATACAAACAATGTGTCTACTATCCCGCGGGGCGCACCCACATCTTGTGTC	2547
QY	754	LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAla	773
DB	2548	CGGCAGCAGGGAACCCCTGCGCCACCGAGC-----ATCTACTTGGCCCTTGAAGTGGCCA	2601
QY	774	AspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet	793
DB	2602	GATGGCTCTATGCGCTCAATGGTGAATACACGCTGATGCGCTCCCGCCACAGATGTGTA	2661
QY	794	TyrLysGlyValVal---LeuArgTrpSerGlySerSerAlaAlaLeuGluArgIleArg	812
DB	2662	CTGCCTGGGCGATGACGCTTCGCTGCAGCGGGGCCACTCGAGCTCAGACACACTGTCA	2721
QY	813	SerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeu	832
DB	2722	GGCCATGGGCCACTGGCCGCTTTCACACTGCAAGTCTCTAGTGGGTGGCAACCCCCAG	2781
QY	833	ArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAsnAlaIle	852
DB	2782	GACACAGCTCTCCGATACAGCTTCTCGTGCCCGCGCGACCCCTTCA---ACGCCACGC	2838
QY	853	ProThrPheSerAlaTrpVal-IleGluGlu-----Trp-----	863
DB	2839	CCCACTCCCAAGACTGGCTGCACCGAAGACACAGATTCTGGAGATCTCTGGCGGCGC	2898
QY	864	---GlyGluCysSer-----	870
DB	2899	CCCTGGCGGGCAGGAATAACTCATATCCCGGCTGCCCTTCTCGGCACCGGGCCT	2958

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Qy      870 sGluLeuGlyTrrpGlnArg- - - - -LeuValGluCysArgAspIleAsnG1 886
Db      2359 CGGACITTAGCTGGGAGAAAGAGAGACTTCTGTGTGCTGCTCATGCTAAGACTCAGTGGG 3018
Qy      886 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 906
Db      3019 GAGG- - - - -GGCTGTGGCGTGAGACCTGCCCTCTCTCTGCTCCCTAATGCGCAGG 3069
Qy      906 pHisProCysPro- - - - -GlnTrpGln- - - - -LeuGlyGluTrpSerSerCysSe 921
Db      3070 CTGGCCCTGCGCTGGTGTCTGCCCCGGGAGGAGTGATGGGTTAGTGATGGAAG--GG 3127
Qy      921 rLysThrCysGlyLysGlyTyrlLysLysThrSerLeuLysCysLeuSerHisAspGlyG1 941
Db      3128 GCTCAGACAGACAGCCCTCCATCTAAATGCGCCCTCTGCTGCGGCTCACAGAGGAGG 3187
Qy      941 Y 941
Db      3188 G 3188

RESULT 11
US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6903
; CURRENT APPLICATION NUMBER: US/09/122.126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-122-126B-14

Alignment Scores:
Pred. No.: 3.85e-164 Length: 3250
Score: 1926.50 Matches: 400
Percent Similarity: 53.53% Conservative: 123
Best Local Similarity: 40.94% Mismatches: 325
Query Match: 36.44% Indels: 130
DB: 4 Gaps: 18

US-09-373-658C-126 (1-967) x US-09-122-126B-14 (1-3250)
Qy      5 ValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnHlaGluArg-AL 24
Db      156 GTTCGGCTGCTCCCTGGCCGC- - - - -GGTCGGCCCCGCCCGCCGAC 194
Qy      24 aProGlySerArgSerPheGlyProValProThrLeuLeuAlaAlaLeuLe 44
Db      195 ACCTGCCCGCAGATAAGCCGGCAGCTCCGACT- - - - -GCTGC 233
Qy      44 uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeuValValProG1 64
Db      234 AGCAGCCGCCAGCCCCCGCGGCGAGGAGGTGCAGAGCGAGCCGAGGCT-- 291
Qy      64 uLeuGluArgValProGlyHisGly- - - - -ThrThrArgLeuArgLeuHisAlaPh 81
Db      292 - - - - -CCCGGCCACCCCGCACCCCTGGCGCAGCGCGCAGGAGCAAGGGGCT 338
Qy      81 eAspGlnGlnLeuAsp- - - - -
Db      339 GGTGCAGAAATCATGACCAACTCTACTCCGCGCGGCAAGTGGGTACTCTGCTCTACGC 398
Qy      87 - - - - -LeuAspValProProAspSerSerPheLeuAlaProGlyPh 100

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Db 399 GGGCGCGGAGGTTCTCTTGGACCTGGAGCGAGATGGTTCGGTGGCATTGCTGGCTT 458  
Qy 100 eThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLe 120  
Db 459 CGTG-----CCGCGAGGCGCGGAGTGCGCCTTGGCGCCACCG 500  
Qy 120 uAlaHisCysPheTySerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSe 140  
Db 501 GAGCCACTGCTTATCTATCGGGGACAGTGGACGCTAGTCCCGCTCTCTGCTGTCTTGA 560  
Qy 140 rLeuGlyGluGlyValArgGlyAlaPheTyLeuLeuGlyGluAlaTyPheIleGlnPr 160  
Db 561 CCTCTGTGGGGTCTTCAGCGCTCTTTCGGGTCACAGCGCGCTACACCTAAAGCC 620  
Qy 160 oLeu-----ProAlaAlaSerGlu-----166  
Db 621 ACTGCTCGCGGACCTTGGCGCGAGGAAGAAAGCGCGGTGTACGGGGATGGGTCCGC 680  
Qy 167 ArgLeu-AlaThrAla-----Alap 173  
Db 681 ACGGATCTCGACGTCTACACCCGCGAGGCTTTCAGTTCGAGCGCCTCGCGCGCGCG 740  
Qy 173 rGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyA 193  
Db 741 CACCTCGGAACCCCGCGCTCCA-----763  
Qy 193 spValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLeAlaGluT 213  
Db 764 -----CACCGGAGCGCCACGAGCATCTCCGCG 791  
Qy 213 hrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTyrSerProGlnA 233  
Db 792 GC-----ACAGCAACCGCGGAGCGCGGACACTGG---CCTCGCA 830  
Qy 233 spProAlaLeuGlnGlyValGlyGlnProThrGlyThr-----GlySerI 248  
Db 831 GCTCTTGGACCACTGCTCTCTCGCGCGCTCGGGGCTCAGGACCGCAGACGTGTGGCG 890  
Qy 248 leArgLysLysArgPheValSerSerHisArgTyValGluThrMetLeuValAlaAspG 268  
Db 891 G-CGGCGCGCGCTCCATCTCCCGCGCGCGCGAGGTGCTGTCTGTGGCTGACG 949  
Qy 268 lnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyLeuLeuThrLeuPheSerV 288  
Db 950 CGTCCATGGCGGTGTATGCGCGCGCTGCGAGCATTAACCTGCTCACCTGGCCTCCA 1009  
Qy 288 alAlaAlaArgLeuTyLysHisProSerIleArgAsnSerValSerLeuValValVal 308  
Db 1010 TCGCCAATAGCGCTGTACAGCCATGCTAGCATTCAGAACCAACATCCGCTGGCGTGGTGA 1069  
Qy 308 ystIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuT 328  
Db 1070 AGTGTGTGTGTAGGCGACAAGGACAGAGCGCTGGNAGTGGACAGAACGCTGCCACCA 1129  
Qy 328 hrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaG 348  
Db 1130 CACTCAAGAACTTTTGAAGTGGCGAGCACCAACACACACACACAGCTGGAGATGACCATGAG 1189  
Qy 348 luhIstYrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysA 368  
Db 1190 AGCACTACGATGAGCTATCTGTTACTCGGAGGATTTATGTGGCATCATTCATG 1249  
Qy 368 spThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValI 388  
Db 1250 ACACCTTGGGAATGGCAGAGCTTGGGACCATATGTTCTCCAGAGCGCAGCTGTGTGTGA 1309  
Qy 388 leGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhea 408  
Db 1310 TTGAAGACGATGGCCTCCAGCGACCTTCACTGTGGCTTCAGAAATCGGACATTTACTTG 1369  
Qy 408 snMetProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerH 428  
Db 1370 GCCTCTCCCAAGGATTCCAAATTCGTGAGAGACCTTTGGTTCCACAGAGATAAGC 1429

Qy 428 isMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerG 448  
Db 1430 GCTTAATGCTTCCATCTTACCAGCATTGATGATCTTAAGCCCTGGTCAATGACACTT 1489  
Qy 448 lyTyMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProG 468  
Db 1490 CAGCCACCATCAGAAATCTCTGGATGATGGCATGTAATGTTGTTGCTGACCTACCA 1549  
Qy 468 lnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyAspAlaAsnArgGlnC 488  
Db 1550 GAAAGCAGATCTGGGCGCGGAAAGAACTCCAGGACAGACCTACGATGCCACCCAGCAT 1609  
Qy 488 ysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 508  
Db 1610 GCAACCTGACATTCGGGCTGAGTACTCGGTGTGTC---GGCATGGATGCTGTGCTC 1666  
Qy 508 hrLeuTrpCysThrGlyThrSerGlyValValLeuValCysGlnThrTyHisPheProT 528  
Db 1667 GCCTGTGTGCTGTGTGCTGACCCAGGCGCAGATGCTGTCTGTGACCAAGAAGTGCCTG 1726  
Qy 528 rpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnL 548  
Db 1727 CGGTGGAAGGAGCGCTTGTGAAAGGGGAGAAATCTGCTGAGGGCAATGTTGTGGACA 1786  
Qy 548 ysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProT 568  
Db 1787 AAACCAAGAAATAATATTATTCAACTCAAGCCATGGCACTGGGGATCTTGGGATCCT 1846  
Qy 568 rpGlyAspCysSerArgThrCysGlyGlyValGlnTyThrMetArgGluCysAspA 588  
Db 1847 GGGGCGAGTGTCTGCTCATCTGGAGGAGGAGTGCAGTTTGCCTATCTGCTCACTGTAATA 1906  
Qy 588 snProValProLysAsnGlyGlyTyTrpCysGluGlyLysArgValArgTyArgSerC 608  
Db 1907 ACCCTGCTCCCAAGAAACAGCGACCTACTGTCAGGGGAAGAGGCCATCTACCGCTCT 1966  
Qy 608 ysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluA 628  
Db 1967 SCAGTCTCATGCTGCCGCCACCC---AATGTAATAATCATTTGCTCATGAACAGTGTGAG 2023  
Qy 628 lhiAsnGlnPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProL 648  
Db 2024 CAAATAATGGCTATCAGTCTGATGCAAAAGGAGTCAAACTTTTGGGAATGGTTCCCA 2083  
Qy 648 ystYrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleG 668  
Db 2084 AATATGCAAGTGTCTCGCCAGCGGATGTGTGCAAGCTGACCTGCAGAGCCAAAGGCACTG 2143  
Qy 668 lyTyPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerT 688  
Db 2144 GCTACTATGTGTATTTTCTCAAAAGTGACCGCATGGCACTGAATGTAGGCCGTACAGTA 2203  
Qy 688 hrSerValCysValGlnGlnCysValLysAlaGlyCysAspArgIleLeuAspSerL 708  
Db 2204 ATTCTGCTGCTGCGGGAGGTGTGTGAGAACTGGCTGTGACCGCATCATTTGGCTCAA 2263  
Qy 708 ystLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleS 728  
Db 2264 AGCTGCAGTATCAAGTGGCGAGTATGTGGAGGACAACTCCAGCTGTACAAAGATTG 2323  
Qy 728 erGlySerValThrSerAlaLysProGlyTyThrHisnspIleIleThrIleProThrGlyA 748  
Db 2324 TTGGAAACCTTTAATAAGAAAAGTAAAGGTTTACCTGACGTGGTGAGGATTCCTGAAGGG 2383  
Qy 748 lhrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheL 768  
Db 2384 CAACCCACATAAAGTTCGACAGTTCARAGCCAAAGACCAGACTAGATTCACTGCTATT 2443  
Qy 768 euAlaIleLysAlaAlaAspGlyThrTyTrpIleLeuAsnGlyAspTyThrLeuSerThrL 788  
Db 2444 TAGCCCTGAAAAAGAAAACCGTGTACTCTTATCAATGGAAGTACATGATCTCCACTT 2503



QY 388 leGluAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheA 408  
DB 1310 TTGAAGAGGATGGCTCCAGGAGCTTCACTGGCTCAGGAATCGGACATTTACTTG 1369  
QY 408 snMetProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerH 428  
DB 1370 GCTCTCCCATGAGATTCGAATTCGTGAAGAGACCTTTGGTTCCACAGAGATAAGC 1429  
QY 428 isMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTppSerProCysSerG 448  
DB 1430 GCTTAATGCTTCCATCTCCAGCATGATGATCATCTAAGCCCTGGTCCAATGCACTT 1489  
QY 448 lyTyrMetThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProG 468  
DB 1490 CAGCCACCATCAGAGATTCCTGGATGAGTGGATGATGATGATGATGATGATGATG 1549  
QY 468 laAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnC 488  
DB 1550 GAAAGCAGATCTGGGCCCGGAGAACTCCAGACAGACCTACGATGACCCAGCAT 1609  
QY 488 ysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerT 508  
DB 1610 GCAACCTGACATTCGGGCTGAGTACTCGGTGTGTC---GGCATGATGTCGTGCTC 1666  
QY 508 hrLeuTppCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProT 528  
DB 1667 GCTGTGGTGTGCTGTGGACGCGGCGGAGATGCTGTGTCGACCAAGAGCTGCTG 1726  
QY 528 rpAlaAspGlyThrSerCysGlyGluGlyLysTppCysIleAsnGlyLysCysValAsnL 548  
DB 1727 CGGTGAAGGAGCGCTTGTGGAAAGGGGAGATCTGCTGCGAGGCGCAATGTGGACA 1786  
QY 548 ysAsnHisArgLysHisPheAspThrProPheHisGlySerTppGlyMetTppGlyProT 568  
DB 1787 AAACCAAGAAATATTTCAACGTCAGGCGCATGCGCAACTGGGGATCTTGGGATCT 1846  
QY 568 rpGlyAspCysSerA-gThrCysGlyGlyValGlnTppThrMetArgGluCysAspA 588  
DB 1847 GGGGCGAGTGTCTGCTCATGTGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 1906  
QY 588 snProValProLysAsnGlyLysTyrCysGluGlyLysArgValA-gTyrArgSerC 608  
DB 1907 ACCCTGCTCCCAACAAACAGGAGCTACTGCGACAGGAGAGGCGCATCTACCGCTCT 1966  
QY 608 ysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluA 628  
DB 1967 GCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2023  
QY 628 laHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTppIleProL 648  
DB 2024 CCAAAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2083  
QY 648 ysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleG 668  
DB 2084 AATATGAGTGTCCTGCCAGCGATGTGTGCAAGCTGACCTGCGAGCGCAAGGCGCATG 2143  
QY 668 lyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerT 688  
DB 2144 GCTACTATGTGTATTTCTCCAAAGGTGACGATGCTGATGCTGATGCTGATGCTG 2203  
QY 688 hrSerValCysValGlnGlyCysValLysAlaGlyCysAspArgIleIleAspSerL 708  
DB 2204 ATTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2263  
QY 708 ysLysLysPheAspLysCysGlyValCysGlyValAsnGlySerThrCysValLysLys 728  
DB 2264 AGTCGAGTATGACAGTGGGAGTATGTGGAGAGACAACTCCACCTGCTGACAAAGTTG 2323  
QY 728 erGlySerValThrSerAlaLysProGlyTyrHisAspIleThrIleProThrGlyA 748  
DB 2324 TTGCAACCTTTAATAAGAAAAGTAAGGGTTTACTCACTGACGTGGTGGAGATTCTCGTGAAGGG 2383

QY 748 laThrAsnIleuValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheL 768  
DB 2384 CAACCCATATAAGTTCCAGAGTTCAAAAGCCAAAGACAGAGACTAGATTCACTGCTATT 2443  
QY 768 euAlaIleIysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrL 788  
DB 2444 TAGCCCTGAAAGAAAGAAACGGTGAGTACCTTATCATGGAAGTACATGATCTCCACTT 2503  
QY 788 euGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaL 808  
DB 2504 CAGAGACTATCATTCACATCAATGAAACAGTCAATCAATATAGCGGTTGGAGCCAGGG 2563  
QY 808 euGluArgIleArg-----SerPheSerProLeuLysGluProLeuThrIleGlnValL 826  
DB 2564 ATGACTTCTCTCATGCGCTACTCTGCGACCAAGAAATCTAATAGTGCAGATTCT 2623  
QY 826 euThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLysL 845  
DB 2624 TTGCAACAGACCCCACTAAACCATAGATGTCGTTATAGCTTTTGTGTTCCCAAGACT 2683  
QY 845 ysLysGluSerPheAsnAlaIleProThrPheSerAla----- 857  
DB 2684 CCACCTCCAAAAGTAAACTCTGCTACTGTCATGTCGCGAGCAATAAAGTGGATCACACTT 2743  
QY 858 -----TppValIleGluGluTppGlyGluCysSerLysSerCysGluLeuGlyT 874  
DB 2744 CCGACCCGCGAGTGGTCAAGGCCCATGGCTGCTCTAGGACTGTGACACAGGTT 2803  
QY 874 rpGlnArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaL 894  
DB 2804 GGCACACAGAACCGTGCAGTGCAGGATGGAACCGGAAGTTAGCAAAAGGATGCTCTC 2863  
QY 894 ysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 909  
DB 2864 TCTCCAAAGGCTTCTGCTTAAAGCAATGCTTGTGAAGAAATGT 2910

RESULT 13  
US-09-369-364A-1  
; Sequence 1, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurskainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3002  
; TYPE: DNA  
; ORGANISM: mus musculus ADAMTS-5  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (18)..(2810)  
US-09-369-364A-1

Alignment Scores:  
Pred. No.: 1,17e-162 Length: 3002  
Score: 1909.50 Matches: 393  
Percent Similarity: 56.83% Conservative: 127  
Best Local Similarity: 42.95% Mismatches: 314  
Query Match: 36.12% Indels: 82  
DB: 4 Gaps: 19

US-09-373-658C-126 (1-967) x US-09-369-364A-1 (1-3002)

QY 70 GlyHisGlyThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspVal 89  
DB 267 GCGCGTGGCAAGTGGGTACTCTTCTACGCGGGCGCGGAGGTCTCTGTCGACCTG 326





Db 2400 TCAGAGACCATCATCGACATCAATGTTACCGTCATGAACTACAGTGGATGGAGCCACAG 2459  
Qy 808 LeuGluArgIleArg-----SerPheSerProLeuLysGluProLeuThrIleGlnVal 825  
Db 2460 GATGATTTTTCATCGGGATGGCTATTTCAGCCACAAAAGAAATCCTGATCGTCAGATC 2519  
Qy 826 LeuThrValGlyAsnAlaLeuArgProLysIleLysThrTy-PheVal---LysLys 844  
Db 2520 CTTCGCACAGACCCAACTAAAGCGTAGCGTCCGTTACAGCTTTTGTCCCAAGAG 2579  
Qy 845 LysLysGluSerPheAsnAlaIle-----Pro 853  
Db 2580 ACCACTCAAAAAGTAACTCTGTCATCCAGCCAGCAACAGGTGGGACCACTCT 2639  
Qy 854 ThrPheSerAlaTrpValIleGluGluTrpGlyGlyCysSerLysSerCysGluLeuGly 873  
Db 2640 ACACAGCTCAGTGGGTGACAGGTCCATGGCTGCCTCCAGGACCTGTGACACAGGC 2699  
Qy 874 TrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893  
Db 2700 TGCCACATGAGACCGTGCAGTCCAGGATGGAAACAGAAATAGCTAAAGATGCCTT 2759  
Qy 894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCys---ProGlnTrp 912  
Db 2760 CTCTCTCAGAGGCTTCTGCAATTAAAGCAATGCTGCTGAAGAAATGTTAGCCTGTG--- 2816  
Qy 913 GlnLeuGlyGluTrpSerSerCysSerLys-----Thr 923  
Db 2817 -----GTTTACTCTAA--TGACAAAAAACAACAGAGATCATCGCAGATACAGC 2866  
Qy 924 CysGly-----LysGlyTrpLysThrSerLeuLysCysLeu 936  
Db 2867 TGTTGTGAAGACAGAGCCCTACCCNAAGCACAGAAAGTCATGCTT 2911

## RESULT 14

US-09-369-364A-12  
; Sequence 12, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Kurkainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 5804  
; TYPE: DNA  
; ORGANISM: Homo sapiens ADAMTS-9  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)...(5648)  
; NAME/KEY: misc feature  
; LOCATION: (1406)  
; OTHER INFORMATION: n=T  
; NAME/KEY: misc feature  
; LOCATION: (1563)  
; OTHER INFORMATION: n=T  
US-09-369-364A-12

## Alignment Scores:

Pred. No.:	7e-148	Length:	5804
Score:	1751.50	Matches:	367
Percent Similarity:	51.03%	Conservative:	153
Best Local Similarity:	36.02%	Mismatches:	307
Query Match:	33.13%	Indels:	193
DB:	4	Gaps:	24

US-09-373-658c-126 (1-967) x US-09-369-364A-12 (1-5804)

Qy 77 ArgLeuHisAlaPheAspGlnGlnLeuAspValProProAspSerSerPheLeu 96  
Db 309 CGCTCTCTCGCTTCGGCCACGAGTTTCTATTATCTACCGCCAAATCGCGATTATC 368  
Qy 97 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu--- 115  
Db 369 GCTCCAGTCTCACTGTCCACCTCTCTGGGACGCCGGGGTGAATCAGACCAAGTTTAT 428  
Qy 116 -----ProGluThrAspLeuAlaHisCysPheTy-SerGlyThrValAsnGlyAspPr 133  
Db 429 TCCGAGAGGAGGAGCGCACTAAAGCACTGTTTCTACAAAAGGCTATGTCATACCACTC 488  
Qy 133 oSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyLeuLeuG1 153  
Db 489 CGAGCACAGCGCCGTCATCAGCTCTGCTCAGAAATG----- 525  
Qy 153 yGluAlaTy-PheIleGlnProLeuProAlaSerGluArgLeuAlaThrAlaAlaPr 173  
Db 526 -----AACACAAAATAGCACACAGTAAAGAC 551  
Qy 173 oGlyGlyLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnGlnGlyAs 193  
Db 552 AAGAGAAAACACAGAG-ACAGAAAATGGGGAGAA-----AGGATTAACTGGCTGGTGA 604  
Qy 193 pValGlyGly---ThrCysGlyValValAspGluProArgProThrGlyLysAlaG1 212  
Db 605 CGTAGCAGCATTAATAACAGCGCTTAGCAACAGAGGCATTTCTGCTTATGTAATAAGAC 664  
Qy 212 uThrClnAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProG1 232  
Db 665 GGACAAACAAGAGAAAGAGCCACAG----- 695  
Qy 232 nAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysAr 252  
Db 696 -----AGCACAAAACG 706  
Qy 252 gPheValSerSerHisArgTyValGluThrMetLeuValAlaAspGlnSerMetAlaG1 272  
Db 707 TTTTATCTATCCACCGTTTGTAGAACTCTGGTGGCAGACAAACAGATGGTTTC 766  
Qy 272 uPheHisGlySerGlyLeuLysHisTyLeuLeuThrLeuPheSerValAlaAlaArgLe 292  
Db 767 ATACCATGGAGAAACCTTCAACACTATATTTTAACTTTAATGTCAATGTAGCTCTAT 826  
Qy 292 uTyLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeuVal11 312  
Db 827 CTATAAGACCAAGTATTGGAAATTTAATAATATTGTTTGTGAACCTTAATGTGAT 886  
Qy 312 eHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPh 332  
Db 887 TCATAATGAACAGATGGGCTTCCATATCTTTTAAATGCTCAGACAAACATTAAAAACTT 946  
Qy 332 eCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyAspTh 352  
Db 947 TTGCCAGTGGCAGCATTCGAAACAGTCCA-----GGTGGAAATCCATCATGATAC 994  
Qy 352 rAlaIleLeuPheThrArgGlnAspLeuCys---GlySerGlnThrCysAspThrLeuG1 371  
Db 995 TGCTGTTCTCTTAACACAGACAGGATATCTGAGAGCTCAGCAGCAATGTATACCTTAG 1054  
Qy 371 yMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAs 391  
Db 1055 CTTGCTGAACACTGGGAACCATTTGTGATCTCCCTATAGAAGCTGTTCTATTAGTGAAGATAG 1114  
Qy 391 pGlyLeuGlnAlaAlaPheThrAlaHisGluLeuGlyHisValPheAsnMetProHi 411  
Db 1115 TGGATTGAGTACAGCTTTTACATCGCCCATGAGCTGGGCCATGTGTTTAACTCCCTCA 1174  
Qy 411 sAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAl 431  
Db 1175 TGATGACAAACAACAAATGTAAAGAA---GAAGGAGTTAAGAGTCCCGCAGCATGTCATGGC 1231  
Qy 431 aSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyMetI1 451



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? LENGTH: 2625
? TYPE: DNA
? ORGANISM: Mus musculus ADAMTS-9
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (2)..(2623)
US-09-369-364A-14

Alignment Scores:
Pred. No.: 6,73e-136 Length: 2625
Score: 1613.00 Matches: 341
Percent Similarity: 55.99% Conservative: 145
Best Local Similarity: 39.29% Mismatches: 312
Query Match: 30.51% Indels: 71
DB: 4 Gaps: 26

US-09-373-658C-126 (1-967) x US-09-369-364A-14 (1-2625)

QY 137 AlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyr 156
D 8 GCGGTCAATCAGCTGTCTCGGAATCATGGCCACGCTTCGGCTCTCACGATGGAGATTAT 67
QY 157 PheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLys 176
D 68 TTCATTGAACACAGCTGAGCTCTGTGGATGAGAA-----GAGGTGAAGAGAA 115
QY 177 ProProAlaProLeuGlnPheHisLeuLeuArgArgAsn-----ArgGlnGly 192
D 116 CAAACAAACCC-----CACATTATTATAGGCACACGACCCCTCAGAGGGAACCC 166
QY 193 AspValGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGlu 212
D 167 TCACAGGAAGACGATGCTGTCGACCTCAGAACTCAAAATAGTCACAGTAAGA-CAA 225
QY 213 ThrGluAspGluAspGluGlyThrGluGlyGluAsp----- 224
D 226 GCGGAATATCAGATGCGAAACGAGAACGAGGAGTAATAGCTGCTGACGAGCGGCAC 285
QY 225 -----GluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237
D 286 GCTAAAGACGGTTTGGCAACAAAGGCTCTCTGGCTATAGCAA-----CAGACAAACAA 342
QY 238 GlyValGlyGlnProThrGlyThr-GlySerIleArgLysLysArgPheValSerSerHi 257
D 343 CACAGGGACAG-----ATGGAACCAACAAAGAACCAAGCGCTTCTGTCTTACC 393
QY 257 sArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerG 277
D 394 ACGGTTTGTAGAGGTGATGTTGTGTGTGCTGACACACAGGATGTTTATACCAACGAGCAA 453
QY 277 yLeuLysHisIstYrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSe 297
D 454 CTTCAACATTATATCTTAACTTAAATGCTTATGCTTCTATCTATCTATAAAGACTCAAG 513
QY 297 rIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLy 317
D 514 TATTGGAATTTAATTAATATTGTTATGTAACCTTAGTCTGATTCATATGTAATGAACGA 573
QY 317 sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLy 337
D 574 AGGACCTTACATAAATTTCAATGCTCCAGACACATTAAGAACCTTTGCCAGTGGCAGCA 633
QY 337 sGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheTh 357
D 634 CTCAAAGAAC-----TACTTGGTGGGATTCCAGCACACAGCGCTCTGGTCAC 684
QY 357 rArgGlnAspLeuCysGlySerGln---ThrCysAspThrLeuGlyMetAlaAspValG 376
D 685 AAGGAGAGATATCTGCAGACTCTCAGACAAATGTGCACACCTTAGTCTCTGTGTAAGTGG 744
QY 376 yThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAl 396
D 745 AACCATTTGGACCCCTTACCAGAGCTGTTCCTATTAGTGAAGACAGTGGGCTGAGCACAGC 804
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QY 396 aPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysG 416
D 805 TTTCAATAGCTCAGACCTGGCCATGTGTTTAAATATGCTCAGCATGACAGCAATAA 864
QY 416 nCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAs 436
D 865 ATGCAAGAA---GAAGGAGTTAAGAGTCCCAGCATGTCATGGCCACCAACACTGAAT 921
QY 436 nLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAs 456
D 922 CTACACCAACCCCTGGATGTGTCAAAGTGCACTCGAATAATACATCACTGAGTTCTAGA 981
QY 456 pAsnGlyHisGlyGluCysLeuMetAspLysPro---GlnAsnProIleGlnIleuProG 475
D 982 CACTGGGTACGGAGAGTGTCTGCTGAATCAACCTGCATCCAGGACCTATCTCTTTCCTTC 1041
QY 475 yAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAs 495
D 1042 CCACCTGCCCGGCTTCTCTCAACCTGAATAAACAATGTGAAGTGAATTTTGGCCAGG 1101
QY 495 pSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSe 515
D 1102 CTCTCAAGTGTGCCCC---TATATGATGCACTGACAGCGCTCTGCTGCAATTAATGTGA 1158
QY 515 rGlyGlyValLeuValCysGlnThrLysHisPheProGlnAlaAspGlyThrSerCysG 535
D 1159 TGGAGCACAAAGGCTGCAAGACTCAGCACAGCCCTGGGACATGGAACCCAGTGTGA 1218
QY 535 yGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisSheAs 555
D 1219 GCCTGGAAGACACTGCAAGTTTGATTTTGTT-----CCCAAGAAATGGA 1266
QY 555 pThrPro---PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgTh 574
D 1267 GGCCCTGCAATTTGATGATGCTCTGGGAGGTTGGAGCCACTTTGGGACCTCTCAAGAAC 1326
QY 574 rCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnG 594
D 1327 GTGTGGAGGAGCATCAAAACAGCCATCAGAGAGTCCAAACAGACAGAGCCAAATAATGG 1386
QY 594 yGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysPr 614
D 1387 TGGGAAGTACTGTGTAGGAAGGAGATGAAGTTTCAATCTGTCAACACGAGAGCCCTGCAT 1446
QY 614 oAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLy 634
D 1447 GAAGCAGAG---CGAGACTTCCGAGAGAGGAGTGT---GCTCAC-----TTTGATGG 1494
QY 634 sAlaSerPhe-----GlySerGlyProAlaValGluTrpIleProLysTyrAlaG 651
D 1495 CAAACACTTCAACATCAATGCTCTGCTGCCAGCGTACGCTGCTTCTTAAGTACAGCG 1554
QY 651 yValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePh 671
D 1555 ANTTTGTATGAAGACCGGTCGAAGTTGTTCTGCAGAGTGGCAGGAACACAGCTACTA 1614
QY 671 eValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCy 691
D 1615 CCAGCTCCGAGACAGAGTGTATTCAGCAACCCCTTGTGGCCAGGACACAAATGACATCTG 1674
QY 691 sValGlnGlyGlnCysValLysAlaGlyCysAspArgGlyIleLeaspSerLysLysPh 711
D 1675 TGTCCAAGGCTTTGCGGCAAGCTGTGATGATATATTATTAACCTCAAGAGTCCGAA 1734
QY 711 eAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerVa 731
D 1735 AGATAATGTGGGATTTGTGTGGAGATAATTCTTCATGCAAAACAGTGGCAGGAACATT 1794
QY 731 lThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIl 751
D 1795 TAACTACTGTCCATTATGTTACAATACTGTTGTGCGAAATTCCGGCTGCTACCAAGCAT 1854
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 18, 2004, 18:42:30 ; Search time 947.831 Seconds  
(without alignments)  
4673.735 Million cell updates/sec

Title: US-09-373-658C-126

Perfect score: 5287

Sequence: 1 MQRPEVGGRRKLGSDMGN.....CDLPKPKHIDPCTMAECS 967

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=btosum62  
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Database :

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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#### ALIGNMENTS

RESULT 1  
US-09-989-687-125  
; Sequence 125, Application US/09989687  
; Publication No. US20040002449A1

GENERAL INFORMATION:

; APPLICANT: Hastings, Gregg A.  
; APPLICANT: Ruben, Steven W.  
; TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides  
; FILE REFERENCE: 1489.107000D  
; CURRENT APPLICATION NUMBER: US/09/989,687  
; CURRENT FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 125  
; LENGTH: 4014

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (466)..(3366)  
; OTHER INFORMATION:  
US-09-989-687-125

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3	5232	99.0	4676	14	US-10-105-929-1	Sequence 1, Appli
4	5224	98.8	4309	15	US-10-210-120-57	Sequence 57, Appl
5	5224	98.8	4459	16	US-10-159-563-192	Sequence 192, App
6	5224	98.8	4459	16	US-10-159-563-308	Sequence 308, App
7	5224	98.8	4760	10	US-09-971-429B-17	Sequence 17, Appl
8	5144	97.3	3261	11	US-09-373-658-1	Sequence 1, Appli
9	5144	97.3	3261	11	US-09-989-687-1	Sequence 1, Appli
10	5140.5	97.2	4848	13	US-10-425-114-26851	Sequence 26851, A
11	4287	81.1	4878	12	US-10-152-319A-1840	Sequence 1840, App
12	4287	81.1	4878	16	US-10-191-803-170	Sequence 170, App
13	4277.5	80.9	4180	10	US-09-373-658-20	Sequence 20, Appl
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15	3922	74.2	2184	9	US-09-445-023A-2	Sequence 2, Appli
16	3922	74.2	2184	15	US-10-097-587-2	Sequence 2, Appli
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18	3652	69.1	2184	9	US-09-445-023A-13	Sequence 13, Appl
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21	3411	64.5	9248	10	US-09-373-658-21	Sequence 21, Appl
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23	3303	62.5	3477	9	US-09-803-588-1	Sequence 1, Appli
24	2642	50.0	3445	9	US-09-803-588-9	Sequence 9, Appli
25	2498.5	47.3	2804	16	US-10-093-463-27	Sequence 27, Appl
26	2496	47.2	3446	9	US-09-965-631-7	Sequence 7, Appli
27	2478.5	46.9	2937	13	US-10-275-107-24	Sequence 24, Appl
28	2478	46.9	2853	9	US-09-965-631-3	Sequence 3, Appli
29	2474	46.8	2867	13	US-09-741-151-1	Sequence 1, Appli
30	2461	46.5	2930	17	US-10-311-035-32	Sequence 32, Appl
31	2334	44.1	3715	13	US-10-425-114-26850	Sequence 26850, A
32	2332.5	44.1	3711	17	US-10-283-975A-398	Sequence 398, App
33	2331.5	44.1	3008	10	US-09-373-658-3	Sequence 3, Appli
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35	2271.5	43.0	3638	9	US-09-918-171A-8	Sequence 8, Appli
36	2208.5	41.8	2940	14	US-10-163-316-1	Sequence 1, Appli
37	2190.5	41.4	2469	14	US-10-163-316-3	Sequence 3, Appli
38	2161	40.9	4307	13	US-10-358-283-31	Sequence 31, Appl
39	2161	40.9	4307	16	US-10-191-987-121	Sequence 121, App
40	2156	40.8	4192	15	US-10-247-685-1	Sequence 1, Appli
41	2149	40.6	4407	10	US-09-946-374-316	Sequence 316, App
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Score: 5287.00 Matches: 967  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 11 Gaps: 0

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QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80  
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QY 161 LeuProAlaLeuSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180  
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QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240  
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QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260  
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QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
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QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820  
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QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840  
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QY 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaIleValIle 860  
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Db 2986 TTGTTAAAG 3045  
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QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880  
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QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900  
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QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940  
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## RESULT 2

US-10-115-286-1  
; Sequence 1, Application US/10115286  
; Publication No. US20030166065A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonak, Zdenka  
; Trulli, Stephen  
; Forwald, James  
; Terrett, Jonathan  
; Hastings, Gregg  
; TITLE OF INVENTION: No. US20030166065A1e1 Integrin Ligand ITGL-TSP  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia  
STREET: Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/115,286  
FILING DATE: 04-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/845,496  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-70000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4014 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
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Best Local Similarity: 98.97% Mismatches: 6  
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QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120  
| | | | |  
Db 766 AGCTTCCAGACGCTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAACCCGCTTC 825  
| | | | |  
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140  
| | | | |  
Db 826 GCGCACTGCTTACTACTCGGCAACCGTGAATGGCGATCCAGCTCGGCTGCGCCCTCAGC 885  
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QY 141 LeuCysGluGlyValAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160  
DB 886 CTCTGCGAGGCGTGCAGGCGCCCTTCTACTGCTGGGGAGGGGATTTTCATCCAGCGC 945  
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180  
DB 946 CTGCCGCGCGCAGCGAGCGCTCGCCACCGCCGCCCGGAGAGCGCGCGGCACCA 1005  
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200  
DB 1006 CTACAGTTTCCACTCTCTCGCGCGGAATCGGAGGCGCGACGTAGCGGCGACGCTGGCGGGTTC 1065  
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220  
DB 1066 GTGACGACGAGCGCCCGCGCCACTGGGAAAGCGGAGACCGAGACGAGCGGAGCT 1125  
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240  
DB 1126 CAGGCGGAGGACGAGGCGCTCAGTGTGCGCGGAGGACCGGCACTGCAAGGCGGTAGGA 1185  
QY 241 GlnProThrGlyThrGlySerIleArgGlyLysArgPheValSerSerHisArgTyrVal 260  
DB 1186 CAGCCACAGAACCTGGAGCATAGAAAGAGCGATTTGTCTCAGTCCCGCTATGTG 1245  
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280  
DB 1246 GAAACCATGCTGTGGCAGACCGAGTCGATGCGAGATTTCCACGCGCAGTGTCTAAAGCAT 1305  
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300  
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QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320  
DB 1366 TCAGTTAGCTGTGGTGTGAAGATCTGTGTCATCCACGATGACAGAGGCGCCGGA 1425  
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340  
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QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360  
DB 1486 CCACCCAGTGACCGGATGCGAGGACATATGACACAGCAATCTTTTCCACGACAGGAC 1545  
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380  
DB 1546 TTGTGTGGTCCACACATGTGATACTCTGGGATGGCTGATGTGGAACCTGTGTGTAT 1605  
QY 381 ProSerArgSerCysSerValIleGluAspGlyLeuGlnAlaAlaPheThrAla 400  
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QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420  
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QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440  
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DB 1786 CAGCCTTGTCTCTCTGTCAGTGCCTACATGATTACATCATTTCTGGATAATGGTCATGG 1845  
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480  
DB 1846 GAAATCTTGTGATGGACAAGCCTCAGAATCCCATACAGCTCCCGAGCGATCTCCCTGGCACC 1905  
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
DB 1906 TCGTACGATGCCACCGGAGTGCAGTTTACATTTTGGGAGGACTCCCAACACATGCGCT 1965

QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520  
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QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540  
DB 2026 TGTCAAAACCAACACATTCCTCGTGGGGGATGGCAGCAGCTGTGGAGAAGGAATGTGTGT 2085  
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DB 2206 TACAGATGAGGAATGTGACAAACCGAGTCCCAAGATGGAGGAGTACTGTGAAGGC 2265  
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QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640  
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QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660  
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QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyClnCysValLysAlaGly 700  
DB 2506 ACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGACAGTGTGTAAAGCTGGT 2565  
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyLysAsn 720  
DB 2566 TGTGATCGCATCATAGACTCCAAAGAGAGTGTGATAAATGTGTGTTCGCGGGGAAAT 2625  
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740  
DB 2626 GSATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGTCAAAACCTGGATATCATAT 2685  
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760  
DB 2686 ATCATCACAATTCNACTGGAGCCCAACCATCGAAGTGAACAGCGGAACCAAGAGGGA 2745  
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780  
DB 2746 TCCAGGAACAATGGCAGCTTTCTTGGCATCAAAAGCTGCTGATGGCAGATATATCTTAAT 2805  
QY 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800  
DB 2806 GGTGACTACACTTTGTTCACCTTAGAGCAAGACATATATGTACAAAGGTGTGCTTCGAGG 2865  
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820  
DB 2866 TACAGCGCTCTCTCGCGCATTTGGAAGAAATTCGACAGCTTTAGCCCTCTCAAGAGAGCCC 2925  
QY 821 LeuThrIleGlnValLeuThrValGlyAspAlaLeuArgProLysIleLysTyrThrTyr 840  
DB 2926 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACCTAC 2985  
QY 841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860  
DB 2986 TTCGTAAGGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGTCAAT 3045  
QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880

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Db 3106 TGGCGACACATTAAATGACACAGCTGCTTCGAGTGTGCAAGAGAGTGAAGCCAGC 3165  
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920  
Db 3166 ACCAGACCTTGTGACAGACCATCCCTGCCCGCAGTGGCGAGTGGCGAGTGGTCAATGT 3225  
Qy 921 SerLysThrCysGlyLysGlyValLysValSerLeuLysCysValLeuSerHisAspGly 940  
Db 3226 TCTAAGACCTGTGGCAAGAGTTACAAAAGAGAGCTTGAAGTGTCTGTCCTCCATGATGA 3285  
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960  
Db 3286 GCGGTGTATCTCATGAGAGTGTGATCTCTTAAAGAAACCTAAACATTTTCATAGACTTT 3345  
Qy 961 CysThrMetAlaGluCysSer 967  
Db 3346 TGCACAATGGCAGAAATGAGT 3366

## RESULT 3

US-10-105-929-1  
; Sequence 1. Application US/10105929  
; Publication NO. US20020137142A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Goodearl, Andrew D.J.  
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
; FILE REFERENCE: 09404/041001  
; CURRENT APPLICATION NUMBER: US/10105,929  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4676  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (460)...(3360)  
US-10-105-929-1

## Alignment Scores:

Pred. No.:	0	Length:	4676
Score:	5232.00	Matches:	957
Percent Similarity:	99.38%	Conservative:	4
Best Local Similarity:	98.97%	Mismatches:	6
Query Match:	98.96%	Indels:	0
DB:	14	Gaps:	0

US-09-373-658C-126 (1-967) x US-10-105-929-1 (1-4676)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20  
Db 460 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGCGCGAAGCTGGCGACGACATGGGGGAC 519  
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40  
Db 520 GCGAGAGGGGCTCCGGGGTCTCGAGAGCTTGGGGCCGTAACCCAGCTGCTGCTGCTGCC 579  
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60  
Db 580 GCGCGCTACTGCGCGTGTGCGAGCGACTCGGGCGCCCTCCGAGGAGGAGGAGGAGCTA 639

Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80  
Db 640 GTGGTCCCGAGCTGAGCGCGCCCGGACACCGGACACCGCCCTCCGCTCGACGCC 699  
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100  
Db 700 TTGACACAGCTGATNTGGAGCTGCGCCCGACAGCAGCTTTTGGCGCCCGGCTTC 759  
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120  
Db 760 ACCTCCAGAACGTGGCGCGCAAAATCCGGTCCGAGACCGCTTCGCGAAACCGACCTG 819  
Qy 121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140  
Db 820 GGCATCTGTTCTACTCCGCGACCGGTAATGGCGATCCAGCTCGGCTCGCCCGCTCAGC 879  
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160  
Db 880 CTCTGCGAGGGGTGCGCGCGCTTCTACTGCTGGGGAGGCGGTATTTTCATCCAGCCG 939  
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180  
Db 940 CTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCGAGGAGAGCGCGCGCACCA 999  
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200  
Db 1000 CTACAGTTCCACTCTCTCGCGGGAATCGGCGGGCGAGTAGCGGCGACGTGCGGGTC 1059  
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220  
Db 1060 GTGACGACGAGCGCGCGCGCTGGAAGAGCGAGACGGAAGCGAGGAGCGAAGGACT 1119  
Qy 221 GluGlyLeuAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240  
Db 1120 GAGGCGGAGGACGAGAGGCTCTAGTGTGTCGCCAGGACCCGCGCATCGAAGCGTAGGA 1179  
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260  
Db 1180 CAGCCACAGGAAGTGAAGACATGAAGAGAGCGGATTTGTGTCCAGTACCGCTATGTG 1239  
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280  
Db 1240 GAAACCATGCTGTGGCAGACCGAGTGGATGGCGAGAATTCACGCGAGTGTGTAAAGCAT 1299  
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300  
Db 1300 TACCTTCTACGTTGTTTGGTGGCGAGCAGATTGTACAAACACCCAGCATTCGTAA 1359  
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320  
Db 1360 TCAGTTAGCTGTGTGTGTGAAGATCTTGTGTCATCCAGATGAACAGAGGGCGGAA 1419  
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340  
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Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360  
Db 1480 CCACCCAGTGACCGGATGCGAGAGCATATGACACAGCAATTTCTTTTACACACAGGAC 1539  
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380  
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Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400  
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Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440

Db 1720 AATGGTGTGACAGGATTCACATGATGGGTCAATGCTTTCCAACTGACACACAGC 1779  
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Db 1780 CAGCCCTTGGTCTCCTTGCAGTCCACATGATTAATCATTTCTGGATAATGGTCATGGG 1839  
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyValSerProGlyThr 480  
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Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
Db 1900 TCGTACGATGCCAACCGGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1959  
Qy 501 AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVal 520  
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Qy 521 CysGlnThrLysHisPheProTyrAlaAspGlyThrSerCysGlyGluGlyLysTyrCys 540  
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Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560  
Db 2080 ATCAACGGCAGATGTGTGAACAAACCGACACAGAAAGCATTTTGTATACGCTTTTTCATGGA 2139  
Qy 561 SerTyrGlyMetTyrProGlyProTyrGlyAspCysSerArgThrCysGlyGlyValGln 580  
Db 2140 AGCTGGGGAATGTGGGGCCTTGGGAGACTGTTTCAGAACTGTCGGTGGAGAGTCCAG 2199  
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600  
Db 2200 TACACGATCAGGGAATGTGACACACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGC 2259  
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnGlyLysThr 620  
Db 2260 AAACGAGTGGCTCAGATCTGTAACTTGGAGGACTGTTCAGAACTGTTCAGAACTGTTCAGAA 2319  
Qy 621 PheArgGluGlnGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640  
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Qy 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyValAsn 720  
Db 2560 TGTGATCCATCATAGACTCCAAAGAGAGTTTGTATAATGTGGTGTGGGGGAAT 2619  
Qy 721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740  
Db 2620 CGATCTACTTGTAAAGAAATATCAGGATCAGTTACTAGTGCAGAAACCTCGATATCATGAT 2679  
Qy 741 IleIleThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGly 760  
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Db 2740 TCCAGGAACAATGGCAGCTTTCTGCCATCAAGCTGTGTGTCGATGGCAGATATATTCTTAAT 2799  
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Db 2800 GGTGACTACACTTTGTCCACTTAGACCAAGACATTATGTACAAGGGTGTGTCTTGAGG 2859  
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Db 3160 ACCAGACCTTGTGACAGACCATCCCTGCCCGGTGGCAGCTGGGGAGTGTGTATCTGT 3219  
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Db 3220 TCTAAGACCTGTGGGAAGGGTTCAAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGA 3279  
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RESULT 4  
US-10-210-120-57  
; Sequence 57, Application US/10210120  
; Publication No. US20030175736A1  
; GENERAL INFORMATION:  
; APPLICANT: Chinnaiyan, Arul M.  
; APPLICANT: Rubin, Mark A.  
; APPLICANT: Sreekumar, Arun  
; TITLE OF INVENTION: Expression Profile of Prostate Cancer  
; FILE REFERENCE: US/10/210,120  
; CURRENT APPLICATION NUMBER: 2002-08-01  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 60/309,581  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: US 60/334,468  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 57  
; LENGTH: 4309  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-210-120-57  
Alignment Scores:  
Pred. No.: 0 Length: 4309  
Score: 524.00 Matches: 956  
Percent Similarity: 99.28% Conservative: 4  
Best Local Similarity: 98.86% Mismatches: 7  
Query Match: 98.81% Indels: 0  
DB: 15 Gaps: 0  
US-09-373-658C-126 (1-967) x US-10-210-120-57 (1-4309)  
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Db 116 ATGACGCGAGCTGTGCGCGGGGTTCCGGAAGCGCGACAGCTGGCGACGACATGGGGGAC 175  
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Db 176 GCGGAGCGGGCTCCGGGCTTCGCGAGCTTTGGGCGCAGTACCCAGCTGTGCTGCTCGCC 235  
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60  
Db 236 GCGGCGCTACTGGCGGTGTCGAGCGACTCGGCGGCCCTCCGAGGAGGACGAGGAGCTA 295  
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80  
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Db 476 GCGCACTGCTTACTCCGCGACCGTGAATGGCGATCCCAAGCTCGGCTGCGCGCTCAGC 535  
Qy 141 LeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaTyrPheIleGlnPro 160  
Db 536 CTCTCGAGGCGCTGCGCGCGCTTCTACTGCTGGGAGAGCGTATTTCATCCAGCGG 595  
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180  
Db 596 CTGCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCCAGGGAGAGCGCGCGGACCA 655  
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlyAspValGlyGlyThrCysGlyVal 200  
Db 656 CTACAGTTCACCTCTCGCGCGGAATCGCGAGGCGAGCTCGCGCGAGCTCGCGGCTC 715  
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220  
Db 716 GTGACGACGAGCCCGCGGCTGCGGAAAGCGAGACCGAGACGAGGACGAGGAGGACT 775  
Qy 221 GluGlyGluAspGluGlyProGlnThrProGlnAspProAlaLeuGlnGlyValGly 240  
Db 776 GAGGCGGAGACGAAAGGGCTCAGTGTGTCGCGCAGGACCGCGACTGCAAGCGTAGGA 835  
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260  
Db 836 CAGCCCGACGAACTGGAACATAGAAAGACGGAATTTGTGCCAGTCAACGCTATGTG 895  
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280  
Db 896 GAAACCATGCTTGTGCGAGACCATGCTGATGGCAGAAATCCAGCGCAGTGGTCTAAAGCAT 955  
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300  
Db 956 TACCTTCTCAGCTGTGTTTCGGTGCGAGCGAGATGTGCAAAACCCCGCATTCGTAAAT 1015  
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320  
Db 1016 TCAGTTAGCTGTGTTGGTGGTGAAGATCTTGTGTCATCCACCATGAAACAGAAAGGCGCGAA 1075  
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnThrGlnLysGlnHisAsn 340  
Db 1076 GTCACTTCCAAATGCTGCGCTCCTGCGGAACCTTTTGCACACTGGCAGAGCAGCAAC 1135  
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360  
Db 1136 CCACCCAGTGCACCGGATGACAGACACTATGACACAGCAATTTCTTTCACCGACAGGAC 1195  
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380

Db 1196 TTGTGTGGTCCCGACAGATGTGATACTCTTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1255  
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400  
Db 1256 CCGAGCAGAGTGTCTCCGTGATGAAGATGATGTTTCAAGCTGCTTCCACAGCC 1315  
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420  
Db 1316 CATGAATAGGCCACGCTGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1375  
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440  
Db 1376 AATGTGTGAACAGGATTTCCACATGATGGGCTCAATGCTTTTCCAACTGACACAGC 1435  
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460  
Db 1436 CAGCCTTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1495  
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480  
Db 1496 GAATGTTTGTGATGACAAAGCTCAGAAATCCCATACAGCTCCAGGCGATCTCCCTGGCACC 1555  
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
Db 1556 TGTGATGATGCCAACCGCGAGTGCAGATTTACATTTGGGAGAGCTCCAAACACTGCCCC 1615  
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520  
Db 1616 GATGAGCCGAGCACATGTAGCACCTTGTGCTGATCCGCGACCTCTGGTGGGCTGCTGGT 1675  
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysThrCys 540  
Db 1676 TGTCAAAACCAACACTTCCCGTGGCGGATGGCACAGCTGTGGAGAGGAAATGTTGT 1735  
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560  
Db 1736 ATCAACGCGCAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCTTTTCATGGA 1795  
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580  
Db 1796 AGCTGGGAATGCGGGCTTTGGGAGACTGTTCCAGAACGTCGGCTGGAGAGTCCAG 1855  
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyrCysGluGly 600  
Db 1856 TACACCATGAGGAAATGTGACAAACCCAGTCCCAAGAAATCGAGGAGNAGTACTGTGAAGC 1915  
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620  
Db 1916 AAACGAGTGGCTACAGATCTCTGTAACCTTGAGGACTGTCCAGACAAATATGGAATAAC 1975  
Qy 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640  
Db 1976 TTTAGAGAGGAAATGTGAACACACACAGAGTTTTCAAAAGCTTCTTTGGAGTGGG 2035  
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660  
Db 2036 CCGCGGTGAATGATTTCCCAAGTACGTCGCGCTCACCAAAAGCAGAGTGCAGAGCTC 2095  
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680  
Db 2096 ATCTGCCAAGCAAGGATTTGGCTTCTTCTGTTTTCAGCCCAAGTGTGTAGATGTT 2155  
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700  
Db 2156 ACTCAATGTAGCCAGATTTCCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAGCTGT 2215  
Qy 701 CysAspArgIleAlaAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720  
Db 2216 TGTGATCGCATCATAGACTCCCAAAAGAGATTTGATAAATGTGTTTTCGCGGGGAAAT 2275  
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740  
Db 2276 GGATCTACTGTAAAAAATAATATCAGATCAGTACTTAGTGCAGAAACCTTGGATATCATGAT 2335

QY 741 lleileThrIleProThrGlyAlaThrAenilleGluValLysGlnArgAspGlnArgGly 760  
Db 2336 ATCATCAAAATCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGAACAGAGGGA 2395  
QY 761 SerArgAsnAsnGlySerPheLeuAlaLelLysAlaAlaAspGlyThrTyrlleLeuAsn 780  
Db 2396 TCCAGGAAACAATGGCAGCTTTCTTGCCATCAAGCTGCTGATGGCACATATATTCTTAAT 2455  
QY 781 GlyAspTyrlleLeuSerThrLeuGluGlnAspIleMetTyrlLysGlyValValLeuArg 800  
Db 2456 GGTGACTACATTTGTCCACCTTAGAGCAAGACATATATGACAAAGGTGTGTCTTGAGG 2515  
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820  
Db 2516 TACAGCGGTCTCTGCGGCAATGGAAAGATTCGACGCTTTAGCCCTCTCAAGAGGCC 2575  
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrlThrTyr 840  
Db 2576 TTGACCATCCAGGTCTTACTGTGGCAATGCCCCCTTGACCTTAAATTAATACACCTAC 2635  
QY 841 PheValLysLysLysLysGluSerPheAsnAlaLalleProThrPheSerAlaTrpValile 860  
Db 2636 TTCGTAAAGAACAGAGGAATCTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2695  
QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880  
Db 2696 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGACTGGTAGAA 2755  
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900  
Db 2756 TCCCGAGACATTAATGGACAGCTGCTCCGAGTGTGCAGAGGATGAGCCAGCCAGC 2815  
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920  
Db 2816 ACCAGACCTTGTGCAGACCATCCCTGCCCGCCAGTGGCAGCTGGGGGAGTGTCTCATGT 2875  
QY 921 SerLysThrCysGlyLysGlyTyrlLysLysThrSerLeuLysCysLeuSerHisAspGly 940  
Db 2876 TCTAAGACTGTGGGAAGGTTTACAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 2935  
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960  
Db 2936 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTT 2995  
QY 961 CysThrMetAlaGluCysSer 967  
Db 2996 TGCACAATGGCAGAATGCAGT 3016

## RESULT 5

US-10-159-563-192  
; Sequence 192, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 192  
; LENGTH: 4459  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-192

Alignment Scores:  
Pred. No.: 0 Length: 4459  
Score: 5224.00 Matches: 956  
Percent Similarity: 99.28% Conservative: 4  
Best Local Similarity: 98.86% Mismatches: 7  
Query Match: 98.81% Indels: 0  
DB: 16 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-159-563-192 (1-4459)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20  
Db 243 ATGAGCGAGCTGTGCCGAGGGGTTTGGAAAGCCGACAGCTGGGACGACATGGGGAAC 302  
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40  
Db 303 GCGAGCGGGCTCGGGGCTCTCGGAGCTTTGGGGCCGTAGCCACGCTGCTGCTGCTGCC 362  
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60  
Db 363 GCGGCGCTACTGCGCGTGTGCGACGCACTCGGGGCCCTCCGAGGAGGAGGAGGAGCTA 422  
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80  
Db 423 GTGCTGCGGAGCTGGAGCGCGCCCGGACACGCGACACGCGCTCCGCTCGCACGCC 482  
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100  
Db 483 TTTGACGAGCAGCTGTGATCTGGAGCTCGCGCCCGACAGCAGCTTTTGGCGCCCGGCTTC 542  
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120  
Db 543 ACGCTCCAGAACTGTGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAACACCGACCTG 602  
QY 121 AlaHisCysPheTyrlSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140  
Db 603 GCGACATGCTTCTACTCCGCGACCGTGAATGGCGATCCAGCTCGGCTGCGCCCTCAGC 662  
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrlLeuLeuGlyGluAlaTyrlPheIleGlnPro 160  
Db 663 CTCTGCGAGCGGCTGCGGGCGGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGCG 722  
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180  
Db 723 CTGCGCGCGCAGCAGCGCTCGCACCGCCCGCCAGGGAGAGAGCCGCGCGGACCA 782  
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyTyrlThrCysGlyVal 200  
Db 783 CTACAGTTCACCTCTCTGCGCGGGAATCGGCGAGGCGACGTCGCGCGCACGTCGCGGGTC 842  
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220  
Db 843 GTGACGACGAGCCCGCGCTGCGAAAGCGGAGACCGAAGACGAGGACGAGGAGGACT 902  
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240  
Db 903 GAGGCGGAGGACGAAGGGGCTCAGTGTGCGCGCAGGACCGCGGCTGCAAGGCGTAGGA 962  
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrlVal 260  
Db 963 CAGCCACAGGAATCGAAGCATAAGAAAGAGCGATTGTGTCTCAGTCCAGCTATGTG 1022  
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280  
Db 1023 GAAACCATGCTTGTGGCAGACCACTGATGCGAGAAATTCACAGGAGTGTCTAAAGCAT 1082  
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrlLysHisProSerIleArgAsn 300  
Db 1083 TACCTTCTCAGTTGTTTTCGTGGCAGCCAGATTGTACAAACACCCAGCATTCGTAAT 1142  
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320  
Db 1143 TCAGTTAGCTGTGTGTGTAAGATCTTGTGTCTATCCACGATGTAACAGAGAGGGCCGGA 1202



321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340  
1203 GTGACCTCCAAATGTCCTCACTCTCGGAACTTTTGCAACTGGCAGAGCAGCAAC 1262  
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360  
1263 CCACCCAGTGCCTCGGATGCGAGCACTATGACACAGCAATCTTTTCCACGACAGGAC 1322  
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380  
1323 TTGTGTGGTCCCAACAGATGATGATCTCTGGATGGCTGATGTGGAACTGTGTGTGAT 1382  
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaIlePheThrThrAla 400  
1383 CCGAGCAGAGAGCTCTCCGTCATAGAGATGATGTTTACAGCTGCTTCCACACAGCC 1442  
401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420  
1443 CATGAATTAGGCCACGCTGTTTAACTGCCACATGATGATCAAAAGCAGTGTGCCAGCCTT 1502  
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440  
1503 AATGGTGTGAACAGGATTCCTCAATGATGCGCTCAATGCTTTCCAACTGGACACAGC 1562  
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460  
1563 CAGCTTGGTCTCTCTGAGTGGCTACATGATTTACATCAATCTCTGGATAATGTCATGGG 1622  
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480  
1623 GAATGTTTGTAGTGAACAGCCTCAGAACTCCATACAGCTCCAGGCGATCTCCCTGGCACC 1682  
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
1683 TCGTACGATGCCAACCGCAGTGCATTTACATTTGGGGAGGACTCCAAACACTGCCCC 1742  
501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520  
1743 GATGCAGCAGCACATGATGACCTTGTGTGTGTACCGCGACCTCTGGTGGGTGCTGTG 1802  
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540  
1803 TGTCAAAACCAACACTTCCCGTGGCGGATGCGACAGCTGTGGAGAGGAAATGTGT 1862  
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560  
1863 ATCAACGCGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGATACGCTTTTCATGGA 1922  
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580  
1923 AGCTGGGGAATGTGGGGGCTTGGGGAGCTGTCGAGAACTGGAGGAGTACTGTGAAGGC 1982  
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600  
1983 TACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGTACTGTGAAGGC 2042  
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620  
2043 AAACGAGTGCCTACAGATCCTGTAACTTGGAGACTGTCAGACAAATAATGGAAAAACC 2102  
621 PheArgGluGlnCysGluAlaHisAscGluPheSerLysAlaSerPheGlySerGly 640  
2103 TTTAGAGAGGAACAAATGGAAGCACAACAGGTTTTCAAAAGCTTCTTTGGGAGTGGG 2162  
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660  
2163 CCTGGGTGGAAATGGATTTCCCAAGTAGCTGCTGCTCCACAAAGCAGCAGGTGCAAGCTC 2222  
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680  
2223 ATCTGCCAAGCAAGGATTTGGCTACTTCTTCTGCTTTTGGACCCCAAGGTTGTAGATGGT 2282

681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700  
2283 ATCCATGTAGCCAGATTCACCTCTGTCTGTGTCAAGGACAGTGTGTAAAGCTGT 2342  
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720  
2343 TGTGATCGCATCATGACTCCAAAAGAGATTTGATAAATGTGTGTTTCCGGGGGAAAT 2402  
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740  
2403 GGATCTACTTGTAAAAAATATACGATTCAGTCTACTAGTGCAAAACCTCGATATCATAT 2462  
741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760  
2463 ATCATCACAAATTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGGAACCCAGAGCGGA 2522  
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780  
2523 TCCAGGAACAATGGCAGCTTCTTGGCCATCAAGCTGCTGTGTCACATATATTCCTTAAT 2582  
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800  
2583 GGTGACTACACTTGTCCACCTTAGAGCAAGCATTTATGTACAAAGGTGTGTCTTGTGAG 2642  
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820  
2643 TACAGCGGCTCTCTCGGCATTTGGAAGAATTCGCAGCTTTAGCCCTCTTCAAGAGCCCC 2702  
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840  
2703 TTGACCATTCAGTCTTACTGTGGCCANTGCCCTTCGACCTAAATTAATACACCTAC 2762  
841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaIleValIle 860  
2763 TTCGTAAGAAGCAAGAGGAATCTTTCAATGCTATATCCCACTTTTTCAGCATGGGTCAAT 2822  
861 GluLysTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880  
2823 GAAGAGTGGCGGCAATGTTCTAAGTCATGTGAATTCGGTTCGCAGAGAGACTGTGTAGAA 2882  
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900  
2883 TGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTCAAAAGGAAGTGAAGCCAGCCAGC 2942  
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920  
2943 ACCAGACCTTGTGCAGACCATCTCCCTCCCTGAGTGCAGCTGGGGAGTGTCTCATGT 3002  
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940  
3003 TCTAAGACCTGTGGGAAGGTTTACAAAAAAGAAAGCTTGAAGTGTCTGTCCCATGTGA 3062  
941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960  
3063 GGGGTGTATCTCATGAGAGCTGTGATCTCTTAAGAAACCTTAACATTTTCATAGACTTT 3122  
961 CysThrMetAlaGluCysSer 967  
3123 TGCAATATGGCAGATGCACT 3143

## RESULT 6

US-10-159-563-308  
; Sequence 308, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563

; CURRENT FILING DATE: 2002-12-09  
 ; PRIOR APPLICATION NUMBER: US 10/133,937  
 ; PRIOR FILING DATE: 2002-04-25  
 ; NUMBER OF SEQ ID NOS: 444  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 308  
 ; LENGTH: 4459  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-159-563-308

Alignment Scores:  
 Pred. No.: 0 Length: 4459  
 Score: 5224.00 Matches: 956  
 Percent Similarity: 99.28% Conservative: 4  
 Best Local Similarity: 98.86% Mismatches: 7  
 Query Match: 98.81% Indels: 0  
 Ds: 16 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-159-563-308 (1-4459)

QY	1	MetGlnArgAlaValProGluGlyPheGlyArgAlaGlyLeuGlySerAspMetGlyAsn	20
DB	243	ATGCAAGCAGCTGTGCCCCAGGGGTTCCGAAGCGCAAGCTGGCGAGACATGGGGAAC	302
QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40
DB	303	CGGGAGCGGCTCCGGGGTCTCGAGCTTTGGGCCGCTACCCACAGCTGCTGCTCGCC	362
QY	41	AlaAlaLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu	60
DB	363	GGGGCGCTACTGGCGGTGTGCGAGCGACTCGGGCGCCCTCCGAGGAGGACGAGGCTA	422
QY	61	ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHis	80
DB	423	GTGGTGCAGGACTGAGCGCCCGCGGACACGCGGACACCGGCTTCGCGCTGACGCC	482
QY	81	PheAspGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
DB	483	TTTGACCAAGCTGGATCTGGAGCTCGGGCGCCGACAGCAGCTTTTGTGGCGCCCGGCTC	542
QY	101	ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGlnThrAspLeu	120
DB	543	AGCTCCAGAACGTGGGGCGCAATCCGGTTCGAGACCCGCTTCCGGAACCGACCTG	602
QY	121	AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
DB	603	GGGCACTGCTTCTACTCCGGCACCGTGAATGGCAATCCAGCTCGCTGCCGCCCTCAGC	662
QY	141	LeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPheIleGlnPro	160
DB	663	CTCTGGAGGGCGTGGCGGGCGCTTCTACTGCTGGGGAGGCGGATTTTCATCCAGCGG	722
QY	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro	180
DB	723	CTGCCCGCCGCGAGCGAGCGCTCCGCCACCGCGCCCGCCAGGGAGAGCGCGGACCA	782
QY	181	LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyClyThrCysGlyVal	200
DB	783	CTACAGTCTCCCTCTGCGGGGGAATCCGCGAGGGCGACGTGCGGGCGACGTGCGGGGTC	842
QY	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluGlyThr	220
DB	843	GTGGACGACGAGCCCGCGCGAGCTGGGAAGCGGAGACCCGAGAGAGAGAGGACT	902
QY	221	GluGlyGluAspGluGlyProGlnThrSerProGlnAspProAlaLeuGlnGlyValGly	240
DB	903	GAGGGCGAGACGAGAGGGGCTAGTGGTGGCGCGCAGGACCCGCGACTGCAAGCGGTAGGA	962
QY	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
DB	963	CAGCCCCACAGGAATGGAGCATAGAGAGACCGGATTTGTTCAGTCCCGCTATGTG	1022

QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
DB	1023	GAAACCAATGCTTGTGGCAGACCACTGATGGCAGAAATCCACGGCAGTGGTCTAAGCAT	1082
QY	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
DB	1083	TACCTTCTCAGTGTGTTTTCGGTGGCAGCAGATGTTACAAACACCCCGCAGCATTCGTAAT	1142
QY	301	SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
DB	1143	TCAGTTAGCTGGTGGTGGTGAAGATCTTGCTCATCCACGATGAACAGAGAGGCGCGGAA	1202
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
DB	1203	GTGACCTCCAAATGCTGCCCTCACTCTCGGAACTTTTGCAACTGGCAGAGCAGCACAAC	1262
QY	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
DB	1263	CCACCCAGTGCAGCGGATGCAGAGCACTATGACACAGCAATTTCTTTTCCACGACAGAC	1322
QY	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
DB	1323	TTGTGTGGTCCCAGACATGTGATATCTTGGGATGGCTGATGTGTGAACTGTGTGAT	1382
QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla	400
DB	1383	CCGAGCAGAAAGCTGCTCGCTCATAGAAGATGATGGTTTACAAGCTGCCCTTCCACACAGCC	1442
QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu	420
DB	1443	CATGAATTAGCCCAACGCTGTTTAAACATGCCACATGATGCAAGACAGTGTGCCAGCTT	1502
QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
DB	1503	AATGTTGTGAACCAAGGATTCACACATGATGGCGTCAATGCTTTCCAACTGCACACAGC	1562
QY	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
DB	1563	CAGCTTGTGCTCTCTTGCAGTGCCTATCATGATTAATCATTTCTGGATAATGGTCATGGG	1622
QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
DB	1623	GAATGTTGTATGGACAAGCTCAGATCCCATACAGCTCCACAGCGCATCTCCCTGGCAC	1682
QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
DB	1683	TCGTACGATGCCAAACCGCAGTGCCTTACATTTGGGGAGGACTCCAAACACTGCCCTC	1742
QY	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
DB	1743	CATGCAGCCAGCACATGTAGCACTTGTGTGTATACCGGCACCTCTGGTGGGGTCTGTGTG	1802
QY	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
DB	1803	TGTCAAAACAAACACTTCCCGTGGCGGATGGCACCACTGTGGAGAGGAAATGGTGT	1862
QY	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
DB	1863	ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCCCTTTTCATCGA	1922
QY	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
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QY	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly	600
DB	1983	TACAGATGAGGGGAATGTGACAAACCCAGTCCCAAGAAATGAGGGAAGTACTGTGAAGGC	2042
QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
DB	2043	AAACGAGTGGCTACAGATCCTGTAACTTGGAGGACTGTCCAGACAAATAATGGAAAAACC	2102
QY	621	PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly	640

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Db 2103 TTAGAGAGAAACAATGTGAAGCACACACAGAGTTTCAAAAGCTTCCTTTGGAGTGGG 2162
Qy 641 ProAlaValGluTrpIleProLysValSerProLysAspArgCysLysLeu 660
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Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2223 AFTGTGCAAGCCAAAGGCATGTGCTACTTCTCGTTTTCAGGCCCAAGGTGTGAGATGT 2282
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyCysValLysAlaGly 700
Db 2283 ACTCCAATGATAGCCCAATCCACTCTGCTGTGTGCAAGGACAGTGTGTAAGCTGCT 2342
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Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2403 GGATCTACTTGTAAATAATATCAGATCAGTCTAGTTCGCAAAACCTGGATATCATGAT 2462
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
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Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrIleLeuAsn 780
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Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2583 GGTGACTACACTTGTCCACTTAGAGCAAGACATATGTACAAAGGTGTGTTCTTGAGG 2642
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2643 TACAGCGGCTCTCTCGCGATTTGGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCCC 2702
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
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Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
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Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
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Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
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Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
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Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
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Qy 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCACATGGCAAGATGAGT 3143
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RESULT 7

US-09-971-429B-17

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: Sequence 17, Application US/09971429B
: Publication No. US20030175704A1
: GENERAL INFORMATION:
: APPLICANT: Lasek, Amy K. W.
: APPLICANT: Shyjan, Andrew W.
: APPLICANT: Turner, Christopher M.
: TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
: FILE REFERENCE: PA-0040 US
: CURRENT APPLICATION NUMBER: US/09/971,429B
: PRIOR FILING DATE: 2001-10-04
: PRIOR APPLICATION NUMBER: 60/239,024
: NUMBER OF SEQ ID NOS: 56
: SOFTWARE: PERL Program
: SEQ ID NO 17
: LENGTH: 4760
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
: NAME/KEY: unsure
: LOCATION: 118
: OTHER INFORMATION: a, t, c, g, or other
: US-09-971-429B-17
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Alignment Scores:
Pred. No.: 0 Length: 4760
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservatives: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 10 Gaps: 0
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US-09-373-658C-126 (1-967) x US-09-971-429B-17 (1-4760)

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Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 621 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCAGTACCCACGCTGCTGCTGCTGCC 680
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 681 GCGGGCGCTACTGCGCGTGTGCGACGCACTCGGCGCGCCCTCCGAGAGGACGAGGAGCTA 740
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 741 GTGGTGCCGAGCTGAGAGCGCCCGGAGACAGGACCCAGCGGCTCGCTTGCAGCGCC 800
Qy 81 PheAspGlnGlnLeuAspLeuAspValProAspSerSerPheLeuAlaProGlyPhe 100
Db 801 TTTGACCAGCAGCTGGATCTGGAGCTGCGGCGCCGACAGCAGCTTTTGGCGCCCGGCTTC 960
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 861 AGCTCCCAAGACGTGGGGGCAAAATCCGGGTCCGAGACCGCCGCTTCCGGAACCCGACCTG 920
Qy 121 AlaHisCysPhePheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
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Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 981 CTCTCGAGCGGTGCGCGCGCTTCTACTGCTGGGGGAGCGGTATTTTCATCAGCGCG 1040
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 1041 CTGCGCGCGCGCGAGCGCTCTGCCACCGCGCGCCCGGAGGAGAGCGCGCGGCGCA 1100
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1101 CTACAGTTCCACTCTCGGGCGGATCGGAGGCGGACGTAGGCGGCAAGTGGGGCTC 1160  
201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220  
1161 GTGGACGACGAGCCCGCGCGACTCGGAAAGCGGAGACCGAAGACGAGGACGAAAGGGACT 1220  
221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240  
1221 GAGGGCGAGGAGGAGGGGCTCAGTGGTCCGCGGAGGACCCGCGCACTGCAGGGCTAGGA 1280  
241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260  
1281 CAGCCACAGGAACCTGGAAGCATAGAAAGAAAGACGATTTGTCTCCAGTCACCGCTATGTG 1340  
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280  
1341 GAACCATGCTTGTGGCAGACCGATCGATGGCAGAAATTCACCGCAGTGGTCTAAGCAT 1400  
281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300  
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1761 CATGAATTAGGCCACATGTTTAAACATGCCATGATGATGATGCAAGCATGTGCCAGCCTT 1820  
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2001 TCGTACGATGCCAACCGGAGTGCAGTTCATTTGGGAGGACTCCAAACACTGCCCC 2060  
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521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540  
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2901 GGTGACTACACTTTGTCCACCTTAGACCAAGACATTAATGACAAAGGTGTGTCTTGAGG 2960  
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 DB 2701 TCATCATCTCTAAGACCTGTGGAGAGGTTTACAAAAAGAGCTTGAAGTGTCTGTCC 2760  
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## RESULT 9

US-09-989-687-1  
 ; Sequence 1, Application US/09989687  
 ; Publication No. US20040002449A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hastings, Gregg A.  
 ; APPLICANT: Ruben, Steven M.  
 ; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
 ; FILE REFERENCE: 1488.107000D  
 ; CURRENT APPLICATION NUMBER: US/09/989,687  
 ; CURRENT FILING DATE: 2001-11-21  
 ; NUMBER OF SEQ ID NOS: 126  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 3261  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(2853)  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3195)  
 ; OTHER INFORMATION: n is any nucleic acid  
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 ; LOCATION: (3248)  
 ; OTHER INFORMATION: n is any nucleic acid  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3255)  
 ; OTHER INFORMATION: n is any nucleic acid  
 ; NAME/KEY: misc feature  
 ; LOCATION: (3261)  
 ; OTHER INFORMATION: n is any nucleic acid  
 US-09-989-687-1

Alignment Scores:  
 Pred. No.: 0 Length: 3261  
 Score: 5144.00 Matches: 940



Percent Similarity: 99.37%    Conservative: 4  
 Best Local Similarity: 98.95%    Mismatches: 6  
 Query Match: 97.30%    Indels: 0  
 DB: 11    Gaps: 0

US-09-373-658c-126 (1-967) x US-09-989-687-1 (1-3261)

18 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 37  
 Db 1 ATGGGAACCGAGCGGGCTCCGGGCTTCGGAGCTTTGGGCCCTTACCCACGCTGCTG 60

38 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57  
 Db 61 CTGCTCCCGCGCGCTACTGCGCGTGTGGACGCACTCGCGCGCCCTCCGAGGAGAC 120

58 GluGluLeuValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArg 77  
 Db 121 GAGGAGCTAGTGTGCGGAGCTGGAGCGCGCCCGGACACGCGCTCCGC 180

78 LeuHisAlaPheAspGlnGlnLeuAspLeuAspValProAspSerSerPheLeuAla 97  
 Db 181 CTGCACGCTTTCACACAGCACTGGATCTGGAGCTGGCGCTCGGCGCCGACAGCCTTTTGGCG 240

98 ProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGlu 117  
 Db 241 CCGGCTTACGCTCCAGAACGTCGGCGCGCAATCCGGGTCGAGACCGCCGCTTCGGAA 300

118 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 137  
 Db 301 ACCGACCTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTTCGGCTGCC 360

138 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 157  
 Db 361 GCCCTCAGCTCTGCGAGGCGGTGCGCGCGCTTCTACTGCTGGGGAGCGGTATTC 420

158 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 177  
 Db 421 ATCCAGCGCTGCCCGCGCACGAGCGCTTCGCCACCGCCCGCCAGGGAGAGCCG 480

178 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 197  
 Db 481 CCGGCAACCACTCAGATTCCACCTCTGCGCGGAAATCGCGGCGCGACGTAGCGCGACG 540

198 CysGlyValValAspAspGluProArgProThrGlyValAlaGluThrGluAspGluAsp 217  
 Db 541 TGGGGGTCTGTGACGACGAGCGCCCGCCCTCTGCGCGGAAATCGCGGCGCGACGTAGCGCGACG 600

218 GluGlyThrGluGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237  
 Db 601 GAAGGAGCTCAGGCGGAGGACGAAGGCGCTCAGTGTGCGCGCACGACCGCGCACTGCCAA 660

238 GlyValGlyGlnProThrGlyThrGlySerIleArgGlyLysArgPheValSerSerHis 257  
 Db 661 GCGTAGGACAGCGCCACAGGACTGGAAGCATAGAAGAAAGCGATTTGTGTCAGTCAC 720

258 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 277  
 Db 721 CGTATGTGGAACCATGCTTGTGGCAGACCACTCGATGCGCAGAAATTCACGCGCAGTGT 780

278 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 297  
 Db 781 CTAAGCAATTACCTTCTCAGTTGTTCGCGCGCAGGATTTGTACAAACACCCCGCAGC 840

298 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 317  
 Db 841 ATTCTGAATTCAGTTAGCTGTGTGGTGGAGATCTTGGTCATCCACGATGAACAGAG 900

318 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 337  
 Db 901 GGGCGGGAAGTGAACCTCCAAATGTCGCTCTCTCGGAACTTTTGAACCTGGCAGAG 960

338 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 357

961 CAGCACAAACCCAGTCAGTCGCGGATGACAGACACTATGACACAGCAATTCCTTTCCACC 1020  
 Db 358 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 377  
 Db 1021 AGACAGACTTGTGTGGTCCCGACAGATGATGACTCTTGGGATGGCTGATGTGGAAC 1080

378 ValCysAspProSerArgSerCysSerValIleGluAspGlyLeuGlnAlaAlaPhe 397  
 Db 1081 GTGTGTGATCCGAGCAGAGAGCTGCTCGTCATAGAAGATGATGTTTACAGCTGCCTTC 1140

398 ThrThrAlaHisGlnLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 417  
 Db 1141 ACCACAGCCCATGAATAGCCCACTGTTTAAATGTCATGCCATGATGATGCAAGCAGTGT 1200

418 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 437  
 Db 1201 GCACGCTTAATGGTGTGAACCGAGATTCACATGATGGCTCAATGCTTTCACACTG 1260

438 AspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsn 457  
 Db 1261 GACCACAGCCAGCTTGGTCTCTCTGAGTGCCTACATGATTACATCATTTCTGGATAA 1320

458 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 477  
 Db 1321 GGTGATGGGGAATGTTTGTATGGACAGCTTCAGATCCCATACAGCTCCAGCGGATCTC 1380

478 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 497  
 Db 1381 CCTGGCACCTCTGATGATGCCAACCGCGAGTCCAGTTTACATTTTGGGAGGACTCCAA 1440

498 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 517  
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518 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 537  
 Db 1501 GTGCTGTGTGTCAACCAACCAACACTTCCGCTGGCGGATGGCACCCAGCTGTGGAGGG 1560

538 LysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPro 557  
 Db 1561 AAATGTGTATCAACGGCAAGTGTGTGAACAAACACGACAGAAAGCATTTTGTATACGCT 1620

558 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 577  
 Db 1621 TTTTCATGGAGCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACCTGCGGTGGA 1680

578 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyr 597  
 Db 1681 GGAGTCCAGTACACGATGAGGAAATGTGACAAACCCAGTCCCAAGAAATGGAGGAAATAC 1740

598 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsn 617  
 Db 1741 TGTGAAGGCAACGAGTGGCTTACAGATCTCTGTAACTTTGAGGACTGTCCAGCAATAAT 1800

618 GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 637  
 Db 1801 GGAAAAACCTTTAGAGAGCAACATGTGAAGCACACACAGAGTTCCTTCAAAAGCTTCCTT 1860

638 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 657  
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658 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 677  
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678 ValAspGlyThrProCysSerProAspSerThrSerValGlnGlyGlnCysVal 697  
 Db 1981 GTAGATGTTACTTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGA 2040

698 LysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCys 717  
 Db 2041 AAAGCTGTTGTGATCGCATCATAGACTCCCAAAAGAGATTGTGATTAATGTGGTGTTC 2100

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QY 738 TyrHisAspIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 757
DB 2161 TATCATGATATCATCAATTCACATTCAGTGGAGCCCAACATCGAAGTGAACAGCGGAAC 2220
QY 758 GlnArgLysArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 777
DB 2221 CAGAGGGATCAGGAAACATGGCAGCTTCTTGCCATCAGAGCTGCTGATGGACATAT 2280
QY 778 IleLeuAsnGlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 797
DB 2281 ATTCTTAATGGTGACTACATCTTGTCCACCTTAGAGCAAGACATATGATACAAAGTGTT 2340
QY 798 ValLeuArgTyrSerGlySerAlaAlaLeuGluAlaGluArgSerPheSerProLeu 817
DB 2341 GTCTTGAGGTACAGCGGCTTCCTCTGCGGCATTTGGAAAGAAATTCGCAGCTTTTAGCCCTCTC 2400
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QY 838 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 857
DB 2461 TACACTACTTCTGAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 2520
QY 858 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 877
DB 2521 TGGGTCAATTGAAGATGGGGCGCAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGA 2580
QY 878 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 897
DB 2581 CTGGTAGAATCCCGAGACATTAATGGACAGCTGCTCCGAGTGTGCAAGGAAGTGAAG 2640
QY 898 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 917
DB 2641 CCAGCCAGCACCAGACCTTGTGCAGACCATCCCTGCCCCCACTGGCAGCTGGGGAGTGG 2700
QY 918 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSer 937
DB 2701 TCATCATCTTCTTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTC 2760
QY 938 HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe 957
DB 2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTC 2820
QY 958 IleAspPheCysThrMetAlaGluCysSer 967
DB 2821 ATAGACTTTTGCACAATGGCAGAAATGCAGT 2850

RESULT 10
US-10-425-114-26851
; Sequence 26851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26851
; LENGTH: 4848
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-036-D4_FLI
US-10-425-114-26851
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Pred. No.: 0 Length: 4848
Score: 5140.50 Matches: 956
Percent Similarity: 92.40% Conservative: 4
Best Local Similarity: 92.01% Mismatches: 7
Query Match: 97.23% Indels: 73
DB: 13 Gaps: 1
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US-09-373-658C-126 (1-967) x US-10-425-114-26851 (1-4848)

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QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
DB 502 GCGAGAGCGGGCTCCCGGGTCTCGGAGCTTTTGGCCCGTACCCACGCTGCTGCTGCC 561
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
DB 562 GCGCGCTACTGCGGTGTCGACGCACTCGGGCGCCCTCCGAGGAGGACGAGAGCTA 621
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
DB 622 GTGGTCCGAGCTGGAGCGGCCCGGGACACGGACACCGCGCTCCGCTGCACGCC 681
QY 81 PheAspGlnLeuLeuAspLeuAspValProPheAspSerSerPheLeuAlaProGlyPhe 100
DB 682 TTTACACGAGCTGGAATCTGGAGCTCGCGCCCGACAGAGCTTTTGGCGCCGCGCTTC 741
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
DB 742 ACGTCCAGAACCTGGGGCGCAATCCGGTCCGAGACCGCGCTTCGGAACACCGACTG 801
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
DB 802 GCGCACTGCTTACTCCGCACTGTAATGGGATCCAGCTCGGCTCGGCGCCCTCAGC 861
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 862 CTCTGAGGGCGTGGCGCGCTTCTACTCTGGGGAGGCGTATTTCATCCAGCCG 921
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyLysProProAlaPro 180
DB 922 CTGCGCGCCGAGCGAGCGCTCGCACCGCCCGCCAGGAGAGCGCGCGCACCA 981
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
DB 982 CTACAGTTCCACTCTCTGGCGGAAATCGGACAGGCGAGCTAGGCGGACGCTCGGGGTG 1041
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 1042 GTGGACGAGCGCCCGCGGCTGAGTGGAAAGCGGACCGAGACCGAGCGAGCGGACT 1101
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 1102 GAGGGCGAGGAGGAGGCTCAGTGTGTGCGCAGGACCGCGCACTGCAAGCGTAGGA 1161
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 1162 CAGCCACAGGAACCTGAGAGCATAGAAGAGAGCGATTGTGTCAGTACCCGCTATGTG 1221
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 1222 GAAACCATCTTGTGGCAGACCATGATGATGCGAGAAATTCACGGCAGTGGTCTTAAAGCAT 1281
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
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Db 1282 TACCTTCTCACTGTTGTTTTCGGTGGCAGCCAGGATTGTACAAACACCCAGCATTCGTAAT 1341  
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320  
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Qy 321 ValThrSerAsnAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340  
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Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360  
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Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380  
Db 1522 TTGTGGGTGCCAGACATGTGATCTTTGGGATGGCTGATTTGGAACTGTGTGTGAT 1581  
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400  
Db 1582 CCGAGCAGAAAGCTGCTCCGTATAGAGATGATGTTTACAGCTGCTTCCACACAGCC 1641  
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420  
Db 1642 CATGAATTAGCCACCGTGTATTACATGCCACATGATGATGCAAAAGCAGTGTGCAGCCT 1701  
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440  
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Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460  
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Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAsnLeuProGlyThr 480  
Db 1822 GATGTTTGTAGACCAAGCTCAGATCCATA-CAGCTCCAGCGCATCTCCCTGGCACC 1880  
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500  
Db 1881 TGTAGATGCCAACCGGAGTGCAGTTTACATTTGGGGAGCACTCCAAACACTGCCCT 1940  
Qy 501 AspAlaSerThrCysSerThrIleuTrpCysThrGlyThrSerGlyValLeuVal 520  
Db 1941 GATGCAGCCAGCACATGTAGCACTTGTGGTGTACCGGACCTCTGGTGGGTGTGGTG 2000  
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540  
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Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAsp 555  
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Qy 556 ----- ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGly 569  
Db 2301 GATTTATGTCTCCATTTAGACCCCTTTTCATCGAAGCTGGGAAATGTGGGGCTTTGGGG 2360  
Qy 569 YAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnPr 589  
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Qy 609 nLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHis 629  
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Qy 629 sAnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTy 649  
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Qy 669 rPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSe 689  
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Db 3321 TTCGAGTGTCCAAAGGAAGTGAAGCCAGCAGCACCGACCTTGTGAGACCATTCCTCTG 3380  
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RESULT 11  
US-10-152-319A-1840  
; Sequence 1840, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1840  
; LENGTH: 4878  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_024400  
US-10-152-319A-1840

Alignment Scores:  
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Query Match: 81.09% Indels: 14  
DB: 12 Gaps: 5

US-09-373-658C-126 (1-967) x US-10-152-319A-1840 (1-4878)

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DB 455 ATCCAGCGGGCAGCAGATTTCCGAGGTCTTCAGTCTTCGACACATGCTGTGTCTACTCTCCTC 514

QY 41 AlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57  
DB 515 GCTTCCATAACAAGTCTGTGTGTGGGGCGGCACACGGGCGCCGCCACGGAGGAGAC 574

QY 58 GluGluLeuValValProGluLeuGluArgValProGlyHis-----GlyThrArgLeu 76

DB 575 GAGGAGCTGGTGTGCTCCCTCGCTGGAGCGCGCCCGGGCCACGATTCACCCACACCTCCTC 634

QY 77 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeu 96  
DB 635 CGTCTGGAGCGCTTTGGTTCAGCAGCTGCATCTGAAGTTGACAGCCAGACAGCGGTTCCTTA 694

QY 97 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu--- 115  
DB 695 GCGCTTGGCTTCCCTCCACCTCCAGACGGTGGGGCGAGTCTCTGGTCCGAGGACAGCATCTG 754

QY 116 ---ProGluThrAspLeuAlaHisCysPheThrSerGlyThrValAsnGlyAspProSer 134  
DB 755 GACCCCACTGGGAGCTTGGCCACTGCTTCTACTCTGGACGGTGAACGGTGACCCCGAC 814

QY 135 SerAlaAlaLeuSerLeuGlyValArgGlyValArgGlyAlaPheThrLeuGlyGlu 154  
DB 815 TCGCCCGCGCCCTCAGCTCTGTGAAGGTGTGGCGGTGCTTCTACCTACCAAGGGGAG 874

QY 155 AlaThrPheIleGlnProLeuProAla---AlaSerClnuArgLeuAlaThrAlaAlaPro 173  
DB 875 GAGTTCATTCAGCCAGCGCTTGGCGTGGCCACCGAGCGCTTGGTCCCGCCGACACCG 934

QY 174 GlyLysProProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAsp 193  
DB 935 AAGGAGGAGTCAATCGCACCTCCGCGGTCCACATCTCAGGCGGAGCGCGGGGCGCAGC 994

QY 194 ValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThr 213  
DB 995 GCGCGCGCAAGTGGGTGTGTCAGGAGGAGAGACCTCTGCAACCC----- 1039

QY 214 GluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAsp 233  
DB 1040 -----AGCACTCGGTTCGCGAAGCCAGACACACCCCGACCGCTCTCTCGGAGAC 1093

QY 234 ProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPhe 253  
DB 1094 CCCACTCTCAGGGCGCGGAAAGCCACAGGACCGAGAGCATGAAGAGAGCGCATTT 1153

QY 254 ValSerSerHisArgTrpValGluThrMetLeuValAlaAspGlnSerMetAlaGluPhe 273  
DB 1154 GTGTCCAGCCCCGTATTGTGGAAACCATGCTGTGGTGTGACCGCTCCATGGGTGACTTC 1213

QY 274 HisGlySerGlyLeuLysHisTrpLeuLeuThrLeuPheSerValAlaAlaArgLeuTrp 293  
DB 1214 CAGCGCAGCGCTCTAAAGCATTTACCTTCTAACCTCTTCTCGGTGGCAGCAGATTTTAC 1273

QY 294 LysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHis 313  
DB 1274 AAGCACCCAGCATTTAGGAATTCATTTAGTCTGGTGGTGAAGATCTTTGGTTCATATAT 1333

QY 314 AspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCys 333  
DB 1334 GAGGACGAGAGGACCGGAAAGTTACTTCCAATGCGCTCTCACCTTAGGAATTTCTGT 1393

QY 334 AsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTrpAspThrAla 353  
DB 1394 AGCTGCGAGAAACAGCACACACAGCCCGAGTCCGAGATCCAGAGCAGCATATGACAGCG 1453

QY 354 IleLeuPheThrArgGlnAspLeuGlySerGlySerGlnThrCysAspThrLeuGlyMetAla 373  
DB 1454 ATTCGTCTCACCAGACAGCATTTATGTGGTCCCAACCTGTGACACTCTCGGATGGCT 1513

QY 374 AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeu 393  
DB 1514 GATGTTGGAACTGTATGTGACCCCGAGAGAGCTGTTGGTTCATCGAAGATGATGTTTAA 1573

QY 394 GlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp 413  
DB 1574 CAGGCTGCTTCCACACAGCCCATGATTTGGCCATGTGTTTAAACATGACACACCGATGAC 1633

QY 414 AlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetLaserMet 433

D5 1634 GCCAAGCAGCTCCGCCAGCTTTAAATGGCGTGAGTGGGAGATCCCATCTGATGGCCCTCGATG 1693  
QY 434 LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSer 453  
D5 1694 CTCTCCAGCTTGGACACAGCCAGCCCTCGTCTCTCTGAGTGCTCATATGCTGCACATCA 1753  
QY 454 PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu 473  
D5 1754 TTCTGGACAAACGGCCATGGGGAATGTTGATGGACAAAGCGCAGAACCCCAATCAAGCTC 1813  
QY 474 ProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGly 493  
D5 1814 CCAATCTGATCTTCCCGGTACTCTTACGATGCCAACCGCCAGTGTCACTGATTACCTTCGGG 1873  
QY 494 GluAspSerIysHisCysProAspAlaSerThrCysSerThrIleuTrpCysThrGly 513  
D5 1874 GAGAAATCCACGCACTCCCTCGATGCGCCAGCAGCATGCGATGCCCTGTGTGTCACCTGGC 1933  
QY 514 ThrSerGlyGlyValLeuValCysGlnThrIleHisPheProTrpAlaAspGlyThrSer 533  
D5 1934 ACCTCCGGTGGCTTACTGGTGTGCCAACAACAACACTTCCCTTGGGCGAGATGGCACCGC 1993  
QY 534 CysGlyGluGlyThrCysIleAsnGlyCysValAsnIysAsnHisArgLysHis 553  
D5 1994 TGGCGAAGAGGGAATGGTGTGCAGCGGCAAGTGTGTGAACAAGACCGACATGAAGCAC 2053  
QY 554 PheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArg 573  
D5 2054 TTGTCTACTCTCTTCAATGGAGCTGGGACCGTGGGACCATGGGAGACTGCTCAAGA 2113  
QY 574 ThrCysGlyGlyGlyValGlnTrpMetArgGluCysAspAsnProValProLysAsn 593  
D5 2114 ACCTGTGTGGAGAGTTCAATATACATGAGAGAATGTGACAACCGGTGCCAAGAAGAC 2173  
QY 594 GlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCys 613  
D5 2174 GGGGGGAAGTACTGCGAAGCAACCAAGTCCGCTACAGSTCCCTGTAACTTGAAGGACTGT 2233  
QY 614 ProAspAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSer 633  
D5 2234 CCAGACAATAACCGAANAACATTACAGAGAGCAATGGAGCGGCAATGATGATTTTCC 2293  
QY 634 LysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSer 653  
D5 2294 AAAGCTTCTCTTGGGAATGAACCCAGCGTGGATGGACACCCCAAGTATGTGGCGTCTCG 2353  
QY 654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673  
D5 2354 CCNAGACAGGTGCAAGCTTACCTCGAAGCCCAAGGCAATGGCTACTCTTGTGTTTA 2413  
QY 674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693  
D5 2414 CAGCCCAAGGTGTAGATGGCACTCCCTGTAGTCCAGACTTACTTCTGTGTGTGCAA 2473  
QY 694 GlyGlnCysValLysAlaGlyCysAspArgIleAspSerLysLysLysPheAspLys 713  
D5 2474 GGACAGTGTGAAAGCTGCTGTGATGATCATAGACTCCAAAAGAAAGTTCGATAG 2533  
QY 714 CysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSer 733  
D5 2534 TGTGGCGTTTGTGAGGAATGGCTCCACGTGCAAGAAATATCAGGAACGTCACACTAGT 2593  
QY 734 AlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluVal 753  
D5 2594 ACAAGACCTGGGTATCATGACATTTGCACAAATTCCTGTGGAGCCACCAACATGAAGTG 2653  
QY 754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaIa 773  
D5 2654 AAACATCGTAATCCAGAGGGGATCCAGAAACATAGGAGCTTCTGGCTATTAGAGCTGCA 2713  
QY 774 AspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793  
D5 2714 GATGGTACCTATATTCTGAATGGAACCTTCACTCTGTCCACTCTAGAGCAAGACCTCACC 2773

QY 794 TyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSer 813  
D5 2774 TACAAAGGTTACTGTCTTAAAGATACATGGTTCCTCAGAGCATTTGGAAGAACCCGACG 2833  
QY 814 PheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArg 833  
D5 2834 TTTAGTCCACTCAAGAACCCCTGACCATCCAGGTTCTTATGGTGGGCCATGTCTCTCCGA 2893  
QY 834 ProLysIleLysTyrThrTyrPheValLysLysLysLysLysLysPheAsnAlaIlePro 853  
D5 2894 CCAAAATCACTACACCTATTTATGAAGAAGACACGAGGCCCTTCAACGCTATTCCC 2953  
QY 854 ThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGly 873  
D5 2954 ACATTTTCGGAGTGGGTGATTGAAGAGTGGGGGAGTGTCCCAAGACATGTGTGTCGGT 3013  
QY 874 TrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893  
D5 3014 TGCAGAGAGAGTGGTAGAGTGCAGAGACATTATAGACACCTCTTCTGAATGTGCC 3073  
QY 894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGln 913  
D5 3074 AAAGAAGTCAAGCCAGCCAGTACCAAGACCTTGTGCAGACCTTCTTGCACACCTTGGCAG 3133  
QY 914 LeuGluGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysThrSerLeu 933  
D5 3134 GTGGGGATTTGTCACTTCTTAAACTTGTGGAGAGGGTTATGAAGAGAACCTTGT 3193  
QY 934 LysCysLeuSerHisAspGlyValLeuSerHisAspSerCysAspProLeuLysLys 953  
D5 3194 AAATGTCTGCCATGATGGCGGTGTGTTATCAATAGAGAGCTGTGATCTTTGAAGAAA 3253  
QY 954 ProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967  
D5 3254 CCAAGACATTACATTGACTTTTGCATACTGACACACAGTCAGT 3295

RESULT 12  
US-10-191-803-170  
; Sequence 170, Application US/10191803  
; Publication No. US20040014040A1  
; GENERAL INFORMATION:  
; APPLICANT: MENDRICK, Donna  
; APPLICANT: PORTER, Mark  
; APPLICANT: JOHNSON, Kory  
; APPLICANT: HIGGS, Brandon  
; APPLICANT: CASTLE, Arthur  
; APPLICANT: ELASHOFF, Michael  
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-50900S  
; CURRENT APPLICATION NUMBER: US/10/191,803  
; PRIOR FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,819  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/305,623  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: US 60/369,351  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: US 60/377,611  
; PRIOR FILING DATE: 2002-05-05  
; NUMBER OF SEQ ID NOS: 1140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 170  
; LENGTH: 4878  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM\_024400  
US-10-191-803-170

Alignment Scores:  
Pred. No.: 0 Length: 4878  
Score: 4287.00 Matches: 790

Percent Similarity: 87.17%      Conservative: 59  
Best Local Similarity: 81.11%      Mismatches: 111  
Query Match: 81.09%      Indels: 14  
DB: 16      Gaps: 5

US-09-373-658C-126 (1-367) x US-10-191-803-170 (1-4878)

QY	1	MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn	20
DB	395	ATGCAGCCAGAAGTCCCTTTGGGGTCAAGCAAGCTGAAGCCCTGCTCAGACATCGGGGAC	454
QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla	40
DB	455	ATCCAGCGGCGAGCAAGTTTCGAGCTCTCAGTCTGCACACATGCTGTGTACTCTCTC	514
QY	41	AlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp	57
DB	515	GCTTCCATAAACAATGCTGCTGTGTGCGGGCGCACACGSGGCGCCCAACGGAGGAAGAC	574
QY	58	GluGluLeuValValProGluLeuGluArgValProGlyHis---GlyThrThrArgLeu	76
DB	575	GAGGAGCTGGTGCTCCCTTCGCTGAGGCGCCCGGGGCCACAGATTCCACCACACTCTCT	634
QY	77	ArgLeuHisAlaPheAspGlnLeuAspLeuAspValProAspSerSerPheLeu	96
DB	635	CGTCTGGAGCGCCTTTGGTCAGCAGCTGCATCTGGAAGTTGCAGCCAGCAGCGGTTCTTA	694
QY	97	AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu---	115
DB	695	GGCCTTGGCTTACCCCTCCACACGGTGGGGCGCAGTCTCTGGTCCGAGGCGCAGCATCTG	754
QY	116	---ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSer	134
DB	755	GACCCCACTGGGACCTGGCCCACTGCTTCTACTCTGGCACGGTGAACGGTGAACCCAGC	814
QY	135	SerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGlu	154
DB	815	TCCGGCGCGCGCCCTCAGCTCTGTGAAGGTGTGCGGGTGCCTTCTACCTACAGGCGGAG	874
QY	155	AlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThrAlaAlaPro	173
DB	875	GAGTTCTTCAITCAGCCAGCGCTCGGGTGGCCACCGAGCGCTGTGCCCGCCCAACCG	934
QY	174	GlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAsp	193
DB	935	AAGGAGGAGTCAATCGCACCTCCCGGTTCCACATCTGAGCGAAGGCGGGCGGCGCAGC	994
QY	194	ValGlyGlyThrCysGlyValValAlaAspGluProArgProThrGlyLysAlaGluThr	213
DB	995	GGCGGGCAAAAGTCGGTGTCTGAGCAGAGAGACCTGCCCACCC-----	1039
QY	214	GluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTyrSerProGlnAsp	233
DB	1040	-----AGCAACTCGGGTCGCGAAAGCCAGACACCCCGCAGCTGGCGCTCTCGCGAAC	1093
QY	234	ProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerLeuArgLysArgPhe	253
DB	1094	CCCCTCTCAGGGCGCGGAAGGCCAACAGGACAGGAAGCATAGGAGAGAGCGATTT	1153
QY	254	ValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPhe	273
DB	1154	GTGTCCAGCCCGCGTTATGTGGAAACCATGCTGCTGGCTGACCATGCTGCTGACTTC	1213
QY	274	HisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyr	293
DB	1214	CACGGCAGCGGTCTAAGCATTAACCTTCTAACCCTGTCTCGGTGGCAGCAGATTTTAC	1273
QY	294	LysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHis	313
DB	1274	AAGCACCCAGCATTAAGAAATCAATTAGTCTGGTGTGTGAAGATCTTGGTCAATAT	1333
QY	314	AspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCys	333

Db	1334	GAGGAGCAGAGGGACCGGAAGTTACTTTC	CAATCGCGCTCTCA	CCCTTTAGGAATTTCTGT	1399
QY	334	AsnTrpGlnLysGlnHisAsnProSerAspArgAspAlaGluHisI	TyrAspThrAla	353	
Db	1394	AGCTGGCAGAAACAGCAACAACAGCC	CAGTGCACCGGATCCAGAGCACTATGACACAGCG	1453	
QY	354	IleIeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAsp	ThrLeuGlyMetAla	373	
Db	1454	ATTCTGTGTTTCCACAGACAGGATTTATGTGGCTCC	CACACCTGTGTACACTCTCGGATGGCT	1513	
QY	374	AspValGlyThrValCysAspProSerArgSerCysSerVal	IleGluAspAspGlyLeu	393	
Db	1514	GATGTTGGAACTGTATGTGACCC	CAGCAGAGCTGTCGGTCATCGAAGATGATGGTTTA	1573	
QY	394	GlnAlaIlePheThrThrAlaHisGluLeuGlyHisValPhe	AsnMetProHisAspAsp	413	
Db	1574	CAGGCTGCTCTTCCACACAGCCATGAAATGGG	CCATGTGTTTAACTATGCCACACAGATGAC	1633	
QY	414	AlaIysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSer	HisMetAlaSerMet	433	
Db	1634	GCCAAAGCACTGGCCAGCTTTAAATGGG	GTGAGTGGGATTTCCCATCTCATGTGGCTCGATG	1693	
QY	434	LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSer	GlyTyrMetIleThrSer	453	
Db	1694	CTCTCCAGCTTGGACCAACAGCCAGCCCTGCTCTCT	TGCAGTGCCTACATGGTGCACATCA	1753	
QY	454	PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLys	ProGlnAsnProIleGlnLeu	473	
Db	1754	TTCTTGACCAACGGCCATGGGGAAATGTTT	ATGTAGACAGCCGACGAACCCAAATCAGACTC	1813	
QY	474	ProGlyAspLeuProGlyThrSerTyrAspAlaAsnArg	GlnCysGlnPheThrPheGly	493	
Db	1814	CCATCTGATCTTCCCGGTACTCTTGACGATGCCAA	CCGCCAGTGTCAGTTTTACCTTCGGG	1873	
QY	494	GluAspSerLysHisCysProAspAlaAlaSerThrCys	SerThrLeuTrpCysThrGly	513	
Db	1874	GAGAAATCCAGCACTCCCTCGATGCAACAGCAGAC	ATGCAATGCACTGCTGTGTGCATCTGGC	1933	
QY	514	ThrSerGlyGlyValLeuValCysGlnThrLysHisPhe	ProTrpAlaAspGlyThrSer	533	
Db	1934	ACCTCCGGTGGCTTACTGGTGTGCCAAACAAAC	ACTTCCCTTGGGCGAGATGGCACACGC	1993	
QY	534	CysGlyGluGlyLysTrpCysIleAsnGlyLysCysVal	AsnLysAsnHisArgLysHis	553	
Db	1994	TGCGGAGAAAGGAAATGGTGTGTCAGCGCAAGTGT	GTGAACAAAGACCCGACATGAAGCAC	2053	
QY	554	PheAspThrProPheHisGlySerTrpGlyMetTrp	GlyProTrpGlyAspCysSerArg	573	
Db	2054	TTTGCTACTCTGTTCTATGGGACTGGGACCGTGGG	ACCATGGGGACACTGCTCAAGA	2113	
QY	574	ThrCysGlyGlyValGlnTyrThrMetArgLysCysAsp	AsnProValProLysAsn	593	
Db	2114	ACCTGTGGTGGAGGAGTTCAATATACATGAGAGA	ATGTGCAACCCCGTCCCAAGAAC	2173	
QY	594	GlyGlyLysTrpCysGluGlyLysArgValAlaArgTyr	ArgSerCysAsnLeuGluAspCys	613	
Db	2174	GGGGGAAGTACTTGCAGAGCAAAACAGTCCCGCT	CAGCTCTGTAAACATGTGAGACTGT	2233	
QY	614	ProAspAsnAsnGlyLysThrPheArgGluGluGlnCys	GluAlaHisAsnGluPheSer	633	
Db	2234	CCAGACAATAACGGAAAAACATTCAGAGAGGAC	AATGCCAGCGCGCACAAATCAGTTTTCC	2293	
QY	634	LysAlaSerPheGlySerGlyProAlaValGluTrpIle	ProLysTyrAlaGlyValSer	653	
Db	2294	AAMGCTTCTCTTTGGGAAATGAACCCACGGTGG	AATGGACACCCCAAGTATGTGGCTCTCG	2353	
QY	654	ProLysAspArgCysLysLeuIleCysGlnAlaLysGly	IleGlyTyrPhePheValLeu	673	
Db	2354	CCAAAGGACAGGTGCAGATTACCTCGGAAGCA	AAAGCATTTGGCTATTCTTTGTTTTTA	2413	
QY	674	GlnProLysValValAspGlyThrProCysSerProAsp	SerThrSerValCysValGln	693	
Db	2414	CAGCCCAAGGTGTAGATGGCACTCCCTGACTCC	AGACTCTACTTCTGTCTGTGTGAA	2473	



QY 694 GlyGlnCysValIysAlaGlyCysAspArgIleAlaSerIysIysPheAspLys 713  
Db 2474 GGACAGTGTGTGAAGCTGCTGTGATCGCATCATAGACTCCAAAAGAGTTCGATAAG 2533  
QY 714 CysGlyValCysGlyCysGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSer 733  
Db 2534 TGTGGGGTGTGTGAGGAATGCTCCAGTGCAGAGAAATATCAGAACGGTCACTAGT 2593  
QY 734 AlaLysProGlyTyrHisAspIleIleThrProThrGlyAlaThrAsnIleGluVal 753  
Db 2594 ACAAGACCTGGGTATCATGACATTGTGCACAAATTCCTGCTGGAGCCACCAATGAGTG 2653  
QY 754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaIle 773  
Db 2654 AAACATCGTAAATCCAGGGAGTCCAGAAACATATGGCAGCTTTCTGGCTATTAGAGCTGA 2713  
QY 774 AspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793  
Db 2714 GATGTGACCTATATTCTGAATGGAACCTTCACTCTGTCTCCACTCTAGAGCAAGCTCAC 2773  
QY 794 TyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSer 813  
Db 2774 TACAAGGTACTGTCTTAAGATACAGTGGTTCCTCAGCAGCATTTGGAAGAAATCCGCAGC 2833  
QY 814 PheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArg 833  
Db 2834 TTTAGTCCACTCAAGAACCCCTGACCATCCAGTTCCTATGTTGGGCCATGCTCTCCG 2893  
QY 834 ProLysIleLysTyrThrTyrPheValLysLysLysGlySerPheAsnAlaIlePro 853  
Db 2894 CCCAAATCAAGTACACCTATTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2953  
QY 854 ThrPheSerAlaTyrValIleGluTyrGlyCysSerLysSerCysGluLeuGly 873  
Db 2954 ACATTTTCGAGTGGGTGATTGAGAGTGGGGAGTGTCTCAAGACATGTGTTCCGGT 3013  
QY 874 TrpGlnArgGluValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893  
Db 3014 TGCAGAGGAGAGTGTGTAGAGTGCAGAGACATTAATGAGACACCTGCTTCTGAATGTGC 3073  
QY 894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGln 913  
Db 3074 AAGAAGTGAAGCCAGCCAGTACCAGACCTGTGACAGCTTCTCTGCCCACCTGTGGCAG 3133  
QY 914 LeuGlyGluTrpSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeu 933  
Db 3134 GTGGGGGATGTGTACCATGTCTTAAACTGTGGGAGGGTATTAAGAGAGACCTTG 3193  
QY 934 LysCysLeuSerHisAspGlyValLeuSerHisAspSerCysAspProLeuLysLys 953  
Db 3194 AAATGTCTCTCCATGATGGCGTGTGTATCAATGAGAGCTGTGATCCTTTGAAGAA 3253  
QY 954 ProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967  
Db 3254 CCAAGCATTATGACTTTTGCATCTACTGACACACAGTGTGAGT 3295

## RESULT 13

US-09-373-658-20  
Sequence 20, Application US/09373658  
Publication No. US20030092900A1  
GENERAL INFORMATION:  
APPLICANT: Ituels-Arispe, Luisa  
APPLICANT: Hastings, Gregg A.  
APPLICANT: Ruben, Steven M.  
APPLICANT: Jonak, Zdenka L.  
APPLICANT: Trulli, Stephen H.  
APPLICANT: Fronwald, James A.  
APPLICANT: Terrett, Jonathan A.  
TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
FILE REFERENCE: 1498.1070006  
CURRENT APPLICATION NUMBER: US/09/373,658  
CURRENT FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 125  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 20  
LENGTH: 4180  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Unknown  
US-09-373-658-20

Alignment Scores:  
Pred. No.: 0 Length: 4180  
Score: 4277.50 Matches: 789  
Percent Similarity: 86.65% Conservative: 61  
Best Local Similarity: 80.43% Mismatches: 110  
Query Match: 80.91% Indels: 21  
DB: 10 Gaps: 6

US-09-373-658C-126 (1-967) x US-09-373-658-20 (1-4180)

QY 1 MetGlnArgAlaValPro-----GluGlyPheGlyArgArgLysLeu 14  
Db 372 GTGCAGGTGCGGTGCCATGTCAGCCAAAGTCCCTTTTGGGGTCAAGCAAGCAGAGCCC 431  
QY 15 GlySerAspMetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValPro 34  
Db 432 TCTCCGACATGGGGACGTCCAGCGGCGCAGAGATCTCGGGGCTCTCTGTCCGCACAC 491  
QY 35 ThrLeuLeuLeuAlaAlaA-----LeuLeuAlaValSerAspAlaLeuGly 51  
Db 492 ATGCTGTTGCT 551  
QY 52 ArgProSerGluGluAspGluLeuValProGluLeuGluArgValProGlyHis 71  
Db 552 CGCCCAACGAGGAGATGAGAGCTGTCTGCTGAGCGCTTTGGCCAGCAGCTACATCTGAAGTTG 671  
QY 72 Gly-----ThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspVal 89  
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us-09-373-658c-126.rnpb

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 ; GENERAL INFORMATION:  
 ; APPLICANT: Hastings, Gregg A.  
 ; APPLICANT: Ruben, Steven M.  
 ; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
 ; FILE REFERENCE: 1488.107000D  
 ; CURRENT APPLICATION NUMBER: US/09/989,687  
 ; CURRENT FILING DATE: 2001-11-21  
 ; NUMBER OF SEQ ID NOS: 126  
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 ; SEQ ID NO 20  
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